Human SLIT protein Human SLIT protein Human cDNA SEQ ID Human SLIT protein Human ORFX ORF2855

secreted pro gene 3 encod

immunoglobul secreted pro

CDNA SEQ ID

Human Human Human Human

Membrane-bound pro Human sbgPRO331a p Human PRO1111 poly Human PRO1111 (UNQ

cc359_4 secreted p

Human secreted pro Human gene 3 encod Amino acid sequenc Human membrane ass Human neuronal gui Amino acid sequenc Human PRO227 polyp

neuro

human Human PRO227 Mature Amino acid sequenc

Human sbqTango79a

prote

Drosophila melanog Amino acid sequenc Amino acid sequenc Human PRO293 prote Human hh00149 prot

Human brain-specif

97US-0059119. 97US-0059263. 97US-0063550. 97US-0065186.

17-SEP-1997; 18-SEP-1997; 28-OCT-1997; 12-NOV-1997;

98WO-US19437

17-SEP-1998;

prote polyp respo prote prote

> immune PR0331

Human angiogenesis Human leucine-rich

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Score

Š. Result

PR0331

Human Human Human Human

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score:

Perfect

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database

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anti-inflammatory; anti-autoimmune; anti-diabetic; spondyloarthropathy; T cell-mediated disease; spondyloarthropathy; sclerosis; renal disease; inflammatory myopathy; hemolytic anemia; thromboorytopenia; thyroiditis; diabetes mellitus; demyelinating polyneuropathy; Guillain-Barre syndrome; multiple sclerosis; polyneuropathy; hepatitis; cirrhosis; enteropathy; sclerosing cholangitis; inflammatory bowel disease; Whipple's disease; skin disease; dermatitis; psoriasis; asthma; allergic rhinitis; tumor; food hypersensitivity; urticaria; eosinophilic pneumonia; transplant; pRO331.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inflammatory cell infiltration; immune response; T cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                           AAB31161
AAG67505
ABB60162
AAG67512
AAY13385
AAB80253
                                                                                        AAB23033
AAB23034
ABB10349
AAB23044
AAB43091
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AAE06043
ABB10522
AAU18084
AAY87135
AAE06112
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AAB74705
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AAY13357
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AAB09968
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AAU18035
            AAY66694
AAE09438
AAU12390
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                                                    AAB6521
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 (first entry)
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 Homo sapiens.
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 RESULT
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Novel protein (Clo
Amino acid sequenc
Human PRO331 prote
Human PRO331 prote
                                                                                                       (without alignments)
2080.399 Million cell updates/sec
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2: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
4: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
5: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
6: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
7: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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                                                                                         ; Search time 34.17 Seconds
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                                                                                                                                                        3362
1 MLNKWTLHPQQIMIGPRFNR.....VHEPLLIRMNSKDNVQETQI
             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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Listing first 45 summaries
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AAW85722
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AAY70673
AAU12355
AAU00826
AAB80262
AAB5292
AAB53089

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel composition containing (apart from a carrier or exciplent), a novel PRO245 polypeptide (I), its agonist or antagonist, or their fragments, for modulating: (i) infiltration of inflammatory cells into tissue; (ii) an immune response; or (iii) T cell proliferation. The composition increases or decreases any of the effects (i)-(iii). The products of the invention have anti-inflammatory, anti-autoimmune and anti-diabetic activity. (I), and its (ant)agonists and their fragments, are used to treat immune related diseases, or atthitis, spondyloarthropathies, systemic sclerosis (scleroderma), idopathic inflammatory myopathies, systemic sclerosis (scleroderma), idopathic inflammatory myopathies (dermatomyositis, polymyositis), systemic vasculitis, sarcoidosis, autoimmune pancytopenia, paroxysmal nocturnal hemoglobinutia), autoimmune pancytopenia, paroxysmal nocturnal hemoglobinutia), autoimmune thrombocytopenia (idiopathic thrombocytopenia (idiopathic thrombocytopenia (idiopathic thrombocytopenia (idiopathic thrombocytopenia), thyroiditis (grave's disease, thyroiditis), diabetes mellitus, immune mediated renal disease, chorento demyelinating polyneuropathy, duillain-Barre syndrome, chronic chiopathic damyelinating polyneuropathy, infectious hepatitis and sclerosing cholangitis, inflammatory bowel disease. Confonic active hepatitis, pand other non-hepatorropic viruses), autoimmune mediated skin diseases soluciame multiphere contents contents contents or immune mediated skin disease service and mune mediated skin disease service manner mediated skin disease service and paratrip mediated skin disease service and paratrip demyelinating mediated services syndrome. The paroxiasis pulling skin disease and paratrip mediated services syndrome contents and order and mune mediated services services and paratrips and paratrip demyelinating mediated effects and paratrip demyelinating mediated effects and paratrip demyelinating mediated effects and paratrip demyelinating mediated mediated mediated medi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bullous skin diseases, erythema multiforme, contact dermatitis, psoriasis, sathma, allergic rhintis, atopic dermatitis, food hypersensitivity, urticaria, eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, and transplantation associated diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (graft rejection, and graft-versus-host-disease). (I), its (ant)agonists or fragment can also be used as an adjuvant in treatment of tumors. Antibodies against (I) can also be used for diagnosing such diseases. This sequence represents the human PRO31 protein which is described in
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                                                                                                                                                                                                      Tumas
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                                                                                                                                                                                                      Gurney AL,
97US-0066364.
97US-0066770.
98US-0088026.
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                                                                                                                                    (GETH ) GENENTECH INC.
                                                                                                                                                                                               Goddard A,
                                                                                                                                                                                                                                                                     WPI; 1999-229499/19.
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21-NOV-1997;
24-NOV-1997;
                                                                  04-JUN-1998;
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NGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLG 180 ELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQ 240

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541 AVMLVIFYKMRKQHHRQNHHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYNS
                                                                                                                                                                                                                                                                                    ADLNVTEGMAAELKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQD
                                                                                                                                                                TGMYTCMVSNSVGNTTASATLNVTAATTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP
                                                                                                                                                                                                                    VVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The new human secreted proteins are encoded by polynucleotides obtained from human placents, adult testes, fetal kidney, fetal brain, adult brain, adult brain and adult blood cDNA libraries. The polynucleotides and proteins are predicted to have biological
                                                      NPWNCNCDILMLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell differentiation; immunostimulation; immunosupression; haematopoiesis regulation; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostasis; thrombolysis; receptor; ligand; anti-inflammatory; tumour suppression; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lavallie ER;
Treacy M;
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Racie LA, Spaulding
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                                                                                                                                                                                                                                                                                                                                                                                                                   AAW85722 standard; Protein; 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel protein (Clone AS209_1).
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(GETH ) GENENTECH INC
             25-JUN-1999
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activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Suggested activities include nutritional activity, cytokine and cell cartioud-differentiation activity, immune stimulating (e.g. soliferation/differentiation activity, immune stimulating (e.g. activity, tissue growth activity, haematopoiesis regulating activity, activin/inhibin activity, chemotactic/chemokinetic activity, activin/inhibin activity, cativity, receptor/ligand activity, anti-inflammatory activity, activity, activity, and tumour inhibition activity. The polynucleotides are also stated to be useful for gene therapy. The sequences identified by a secretory leader cativity activity by virtue of their secreted nature. This polypeptide was encoded by a clone designated AS209_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGLANLNTLELFONRLTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLG 180
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2 (2)
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Best Local Similarity 100.
Matches 640; Conservative
                                                                                                                                                    640 AA;
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Secreted protein; transmembrane protein; human; enterocolitis; 2011inger-Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; Alzheimer's disease; Alzheimer is disease; Alzheimer and scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair.
                              sequence of protein PRO331.
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9705-0059265
9705-0059265
9705-0059285
9705-0062816
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(first entry)
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29-0CT-1997;
29-0CT-1997;
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15-OCT-1997;
17-OCT-1997;
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28-OCT-1997;
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                              Amino acid
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AAY13344-403 represent secreted and transmembrane human proteins.

The cDNA sequences are obtained from CDNA libraries, prepared from fetal lung, fetal thiorey, fetal brain, fetal liver and fetal retina.

The ancoded polypeptides have specific uses based on their homology to speciated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions

(e.g. enterocolitis, 20llinger-Ellison syndrome, gastrointestinal mucosa and the repair of acute and chronic mucosal lesions

(e.g. enterocolitis, 20llinger-Ellison syndrome, gastrointestinal microvallus atrophy, skind diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the vulva and gliomas), concers such as lung squamous cell carcinoma of the vulva and gliomas), concers such as lung squamous cell acarcinoma of the vulva and gliomas), content effects on cell growth and development, diseases related to growth or survival of nerve cells including Parkinson's disease, as a target for anti-tumor drugs. PRO533 may be used in the treatment of usher Syndrome or Arrophia areata; PRO565 can be used as an anti-thrombotic agent; PRO387 polypeptides and portions may have threatpeutic applications in wound healing and tissue sepair. PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract.
                                                                                                                                                New isolated human genes and polypeptides used in, e.g. treatment of gastrointestinal ulceration
                          'n
                          Yuan
                       ΜĬ
                       Wood
                       Pennica D,
                                                                                                                                                                                                                            Claim 12; Fig 104; 320pp; English.
                       Gurney AL,
                       Goddard A,
                                                                      WPI; 1999-229533/19.
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                    Chen J,
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Gaps ; 0 100.0%; Score 3362; DB 20; Length 640; 100.0%; Pred. No. 2.3e-234; ive 0; Mismatches 0; Indels 0; Conservative Similarity Query Match Best Local Simi Matches 640;

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                                                                      NGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLG 180
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VVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMA 540

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Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation; diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, anglogenesis and cardiovascularisation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goddard A;
                                              or
Gerber H, Hillan KJ, Godde
Kuo SS, Paoni NF, Smith V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial angiogenic disorders in mammals -
                                                                                             601 YKSPFNHTTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI 640
                                                                                                                                                                                                                                  protein sequence SEQ ID NO:107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ashkenazi AJ, Baker KP, Ferrara N, Godowski PJ, Gurney AL, Klein RD, Watanabe CK, Williams PM, Wood WI;
                                                                                                                                                                AAB24407 standard; Protein; 640 AA
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99WO-US20111.
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99US-0134287.
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99US-0144758
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99WO-US23089
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Williams PM,
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Watanabe CK,
                                                                                                                                                                                                                                   Human PRO331
                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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14-MAY-1999;
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         nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endotherial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24388 to AAB2435 represent nucleotide and protein sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                        NGLANLNTLELFDNRITTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLG 180
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 agonists and antagonists of these
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PRO331; UNQ292; dermatological; immunosuppressive; antiinflammatory; immunostimulant; antiasthmatic; antirhemmatic; antiarthritic; virucide; antiallergic; haemostatic; hepatotropic; antidiabetic; antianaemic; nephrotropic; neuroprotective; anticoagulant; immunological disorder; lung; pneumonia; skin; psorlasis; kidney; glomerulonephritis; arthritis; spondyloarthropathy; SLE; systemic lupus erythematosis; scleroderma; idiopathic inflammatory myopathy; anaemia; thrombocytopenia; diabetee; throidistis; grave's disease; demyelinating disease; multiple sclerosis; graft-versus-host-disease.
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/note= "Casein Kinase II phosphorylation site"
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e= "Casein Kinase II phosphorylation site"
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/note= "cAMP and cGMP-dependent
                                                                                                                                                                                                                                                                            site"
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te= "N-myristoylation site"
                                                                                                                                                           'note= "N-myristoylation site"
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te= "N-glycosylation site"
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.e= "N-glycosylation
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268.272
---- "Casein Kinase I?
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.+o= "Casein Kinase
                                                                                                                                                                                                                                    phosphorylation site"
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N-PSDB; AAS21427
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It enhances or suppresses the infiltration of Inflammatory cells into tissues, proliferation of I-lymphocytes and modulates the immune related alsorders, like SLE, rheumatoid/juvenile arthritis, spondyloarthropathy, systemic sclerosis (scleroderma), idiopathic inflammatory myopathies such systemic sclerosis (scleroderma), idiopathic inflammatory myopathies such as dermatompositis, Slogren's syndrome, vasculitis, sarcoidosis, autoimmune heemolytic anaemia, thrombocytopenia, thyroiditis e.g. Grave's disease, diabetes mellitus, immune-mediated renal disease e.g. cultilain-Barre syndrome, hepatobiliary diseases like hepatitis and cullian-Barre syndrome, hepatobiliary diseases like hepatitis and primary biliary cirrhosis, inflammatory and fibrotic lung diseases such as inflammatory bowel disease (e.g. Crohn's disease), autoimmune or immune-mediated skin diseases such as psoriasis, allergies like asthmà, immunological diseases of the lungs such as posinophilic pneumonia and transplantation associated diseases such as graft-versus-host-disease.
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                                                                                                                                          Composition for treatment and diagnosis of immune related diseases e.g. Grave's disease comprises a PRO245, PRO217, PRO301, PRO266, PRO335, PRO331 or PRO326 polypeptide or its agonists or antagonists (preferably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLG 180
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                                                                Wood WI;
                                                                Gurney AL, Tumas D,
                                                                                                                                                                                                                       Example 1; Fig 14; 201pp; English.
 98WO-US19437
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                               (GETH ) GENENTECH INC
                                                              Goddard A,
                                                                                            WPI; 2000-271435/23.
N-PSDB; AAZ52207.
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17-SEP-1998;
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Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.
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                                                                                      Gao
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NL, Sherwood S;
Nod WI, Zhang Z;
VVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMA
                 AVMLVIFYKMRKOHHRONHHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYNS
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A, Godowski PJ, Gurney AL, Sher
Tumas D, Watanabe CK, Wood WI,
                                                                                                                                     601 YKSPFNHTTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI
                                                                                                                                                       AAU12355 standard; Protein; 640 AA
                                                                                                                                                                                                                                                                                                                                                            Human PRO331 polypeptide sequence.
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99WO-US28564.
99WO-US28565.
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99WO-US30095.
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2000WO-US14941.
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ME, Goddard
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24-FEB-2000;
24-FEB-2000;
01-MAR-2000;
20-MAR-2000;
21-MAR-2000;
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18-FEB-2000;
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16-DEC-1999)
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30-DEC-1999)
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Smith V,
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ANU12172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bloactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, to modulate biological activities of cells expressing pro propagate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor alpha (TNP-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation of chondrocytes, the proliferation of inner ear utricular supporting cells or artilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy. Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. Claim 12; Fig 368; 813pp; English breast, prostate, cervical lung,

640 AA; Sequence

ö ICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAF 120 NGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLG 180 ELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQ 240 GLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHH 300 NPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPP 360 ADLNVTEGMAAELKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQD 420 480 tgmytcmvsnsvgnttasatlnvtaatttpfsyfstvtvetmepsqdearttdnnvgptp 480 541 AVMLVIFYKMRKQHHRQNHHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYNS 600 Gaps 1 MLNKMTLHPQQIMIGPRFNRALFDPLLVVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKV 60 TGMYTCMVSNSVGNTTASATLNVTAATTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP **VVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMA** 0; 100.0%; Score 3362; DB 22; Length 640; 100.0%; Pred. No. 2.3e-234; ive 0; Mismatches 0; Indels 0; Query Match 100. Best Local Similarity 100. Matches 640; Conservative 61 121 361 421 61 181 181 241 241 301 301 361 421 181 181 g qq ŏ g ò q ò a δ g à g ò 셤 g ò ò ò ð

/note= "Glycine is N-myristoylated"

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Human; PRO331; UNO292; immune response; osteoarthritis; systemic sclerosis; systemic lupus erythematosus; rheumatoid arthritis; systemic sclerosis; judicopathic inflammatory; myopathy; polymyositis; systemic vasculitis; arcoidosis; autoimmune haemolytic andemia; immune pancytopaenia; which arcoidosis; autoimmune haemolytic andemia; immune pancytopaenia; whyoriditis; grave's disease; Hashimoto's thyroiditis; diabetes mellitus; glomerulonephritis; demyelinating disease; multiple sclerosis; duillain-Barre syndrome; hepatobiliary disease; whoric inflammatory demyelinating polymeuropathy; infectious hepatitis; auto immune chronic active hepatitis; primary biliary cirrhosis; who inflammatory bowel disease; Crohn's disease; Winple's disease; whiple's disease; which amultiforme; psoriasis; asthma; allergic rhinitis; urticaria; food hypersensitivity; eosinophilic pneumonia, graft rejection; which and the proposition of t
/label= Phosphorylation_site
/note= "cAMP/cGMP dependent protein kinase
phosphorylation site"
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228..234
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te= "Glycine is N-myristoylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immune response protein PRO331 (UNQ292).
                                                                                                                                      ykspfnhtttvntinsihssvhepllirmnskdnvqetqi
                                                                                                      YKSPFNHTTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI
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The sequence represents Human PR0331 (UN0292), a protein involved in the immune response. PRO polypeptides, and (ant)agonists to them, are used in compositions of medulating in inflammatory cells into a tissue, modulating an immune response and modulating proliferation of T-lymphocytes in response to an antigen. Immune related diseases can be treated with the compositions, such as, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthopathies, systemic sclerosis, idiopathic inflammatory compositions, such as moment enempty of autoimmune thrombocytopaenic sclerosis, idiopathic inflammatory autoimmune mediated renal disease, Hashimoto's thyroiditis), autoimmune-mediated renal disease, (e.g. immune pancytopaenic purpura), autoimmune-mediated renal disease, (e.g. immune pancytopaenic purpura), cartoiditis (e.g. Grave's disease, Hashimoto's thyroiditis), diabetes mellitus, immune-mediated renal disease, e.g. immune pancytopaenic purpura), campyelinating diseases of the central and peripheral nervous systems e.g. multiple sclerosis or Guillain-Barre syndrome, and chronic inflammatory cartoidentes and polyneurorpathy, hepatolilary diseases such as infectious cauto immune chronic active hepatitis, primary biliary cirrhosis, disease (ulcerative colitis, Crohr's diseases and Whipple's disease), autoimmune or immune-mediated skin diseases (e.g. erythaemia colitis, crohr's diseases and whipple's disease, food hypersensitivity, immunologic diseases and whipple scolated diseases including graft-versus-host-disease and graft colonophilic pneumonias, idopathic pulmonary fibrosis, transplantation associated diseases including graft-versus-host-disease and graft colonophilic pneumonias, idopathic pulmonary fibrosis, ransplantation of the diseases, to identify publibitors, and to stimulate the proliferation of indiagnosis. PNC polypeptides can be used to detect PRO onlypeptides and the publicates and entiped publication and publicated publication and publication and publicati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition for diagnosing and treating immune related diseases, e.g., rheumatoid arthritis and diabetes mellitus, comprises a PRO polypeptide, agonist, antagonist or fragment -
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'note= "Asn is N-glycosylated"
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/note= "Asn is N-glycosylated"
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Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory; antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant; antiangiogenic; vasotropic; antiashmatic; antirheumatic; cancer; antiarthritic; antiinfertility; antidabetic; antiviral; diabetes; ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
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           ICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAF
                                                         GLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHH
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26-JUL-1999;
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Best Local Similarity 100. Matches 640; Conservative

Similarity

Query Match

Ashkenazi AJ, Filvaroff E, H Godowski PJ, C Mather JP, Pa Williams PM,

PPR R PPR PPR

15-SEP-1999; 15-SEP-1999; 05-OCT-1999; 29-NOV-1999; 30-NOV-1999; 16-DEC-1999;

13-SEP-1999

20-DEC-1999; 20-DEC-1999; 05-JAN-2000;

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                                         ADL.NVTEGMAAELKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQD
                                                                                    TGMYTCMVSNSVGNTTASATLNVTAATTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP
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2000WO-US05004.
2000WO-US05841.
2000WO-US06884.
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99US-0158663
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18-FEB-2000;
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08-0CT-1999;
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01-DEC-1999;
16-DEC-1999;
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06-JAN-2000;
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17-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       transmembrane PRO polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. lung enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia, atherosclerosis), inflammatory disorders (e.g. asthmatoria cardiolastes and retinal disorders such as retinitis pigmentosum. The PRO nucleic acids have applications in molecular biology, including use as hybridization probes, and in chromosome and gene mapping.
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                                                                                                                                                                                                                                                                                                                                          Sixty one nucleic acids encoding PRO polypeptides which are useful ithe treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g.
                                                                                                                                                                                                                Ferrara N;
E, Goddard A;
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Kljavin IJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence is one of sixty one novel secreted and
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99WO-US23089
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                                                                                                                                                                                                                                                                                                                                                                                     Alzheimer's disease)
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N-PSDB; AAF72423.
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Best Local Sim Matches 640;

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Query Match

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                                                                                                                                                                                                                       proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bioactive molecules, such as can be used for targeted delivery of bioactive molecules, such as can be used as radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. Ash44270 to AR44470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAR44087 to AAR44269 and AAB65180 tepresent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
Godowski PJ;
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               Paoni NF;
Wood WL;
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                                                                                                                                                                                                              present invention describes human secreted and transmembrane PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRO polynucleotides used to produce polypeptides used to target bloactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death -
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Goddard A
MA, Pan J
Williams P
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               AL, Kljavin IJ, Napier
Tumas D, Watanabe CK,
   Gerritsen ME,
                                                                                                                                                                              Claim 12; Fig 314; 935pp; English.
 Ħ,
 Gerber
                 Gurney
                             Stewart TA,
                                                                        WPI; 2001-032160/04
N-PSDB; AAF44261.
 Fong S,
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               CJ,
   Perrara N,
                 Grimaldi
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                                               Shang
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The invention relates to novel human angiogenesis-associated proteins designated PRO proteins (AAB53064-B5309), and to nucleic acids encoding PRO proteins. The invention also relates to vectors and host cells comprising a PRO nucleic acid, the recombinant production of a PRO protein, PRO antibodies specific for a PRO protein, fusion process comprising a PRO protein, agonists or antagonists of a PRO protein and compounds which inhibit the expression of a PRO gene. The invention
                                                                                                                                                                                                                                                  cardiac hypertrophy; cardiovascular disorder; endothelial disorder; anglogenic disorder; atherosclerosis; osteoporosis; hypertension; myocardial infarction; diabetic retinopathy; rheumatoid arthritis; Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer; Alzheimer's disease; Huntington's disease; stroke; drug screening;
SA;
                                                                                                                                                                                                                                          Human; angiogenesis-associated protein; PRO; endothelial cell growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid for producing a PRO polypeptide, analyzing genetic disorders and treating cardiovascular, endothelial or angiogenic disorders, such as atherosclerosis, wounds or cancer -
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                                                                                                                                                                                                              Human anglogenesis-associated protein PRO331, SEQ ID NO:137.
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I, Kuo SS, Mar
Williams PM,
                                                   YKSPFNHTTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI
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Watanabe CK, V
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                                                                                                                                  640
                                                                                                                                                                                                                                                                                                                        transgenic animal
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990S-0134287.
99WO-US12252.
99US-0141037.
99US-0144758.
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99WO-US20594.
99WO-US21090.
                                                                                                                                  standard; Protein;
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Paoni NF, Pitti RM,
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N-PSDB; AAC97475.
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                                                                                                                                                                                                                                                                                                                      gene therapy;
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26-JUL-1999;
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08-SEP-1999;
15-SEP-1999;
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14-MAY-1999;
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augiculationally encompasses mechanism in a monthelial or angiogenic disorder, or a susceptibility to such a disorder by detecting mutations in a PRO gene, or the expression level of a PRO gene within a particular tissue; treating a cardiovascular, endothelial or angiogenic disorder via the administration of a PRO protein, PRO nucleic acid, or PRO agonist or antagonist; a retroviral gene therapy vector comprising a PRO agonist or antagonist; a retroviral gene therapy vector comprising a PRO nucleic acid; and methods of inhibiting or stimulating endothelial cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the administration of a PRO protein, or an agonist or antagonist thereof. PRO nucleic acids, PRO protein, or an agonist or antagonist thereof. PRO nucleic acids, PRO protein, or an agonist or antagonist thereof. PRO agonists and PRO antagonists may be used as therapeutic agents to treat cardiovascular, endothelial or angiogenic disorders, such as therosclerosis, osteoporosis, myocardial infarction, hypertension, diabettic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis, endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's disease, or stroke. PRO nucleic acids are additionally useful in the recombinant production of PRO proteins, as hybridisation probes to soreen libraries to isolate cDMAs with sequence identity to PRO proteins, comang genes encoding PRO proteins, a maling gene therapy. PRO nucleic acids can also be used to produce transgenic and an also also and an angle of produce transgenic can also also and also proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cherapeutic agents. The present sequence represents a PRO protein of the
additionally encompasses methods of identifying modulators of PRO
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640 AA; Sequence

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                                                 MLNKMTLHPQQIMIGPRFNRALFDPLLVVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKV
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                                                                                                                                                                                                                                                                     ADLINYTEGMAAELKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQD
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                                                                                                                                                                                                                                                                                                                                               VVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMA
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                      ö
  Length 640;
                      Indels
100.0%; Score 3362; DB 22;
llarity 100.0%; Pred. No. 2.3e-234;
Conservative 0; Mismatches 0:
  Query Match
Best Local Similarity
Matches 640; Conserv
            Best Loca
Matches
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                                                                                                                                                                                                             241
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cell proliferation; differentiation disorder; cancer; neuronal disorder; neurological disorder; demyelinating disease; multiple sclerosis; degenerative disease; Alzheimer's disease; Huntington's disease; spinocerebellar degeneration; nervous system; bone disorder; osteoporosis; immune disorder; rheumatoid arthritis; diabetes mellitus; cardiovascular disorder; liver disorder; viral disease; pain; metabolic disorder; chromosomal mapping; tissue typing; forensic biology; cytostatic; nootropic; neuroprotective; anticonvulsant; osteopathic; antirheumatic; antiarthritic; virucide; analgesic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptide useful for treating cancer, multiple sclerosis,
                                                                                                                                              Human; leucine-rich repeat; LRR; 31939 protein; therapy;
                                                                                                                          Human leucine-rich repeat (LRR) family member protein.
                                                                                                                                                                                                                                                                                                                              "Mature human 31939 protein"
           640
311..362
/label= C-terminal_LRR_domain
378..438
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                                                                                                                                                                                                                                                                                                                                                  N-terminal_LRR_domain
                                                                                                                                                                                                                                                                                                         /label= Signal_peptide 39..713
                                                                                                                                                                                                                                                                                    Location/Qualifiers
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/label= LRR_domain
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                                                             713
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                                                            AAE13006 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US10380
                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      .158
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/label- 1
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                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                   AAE13006;
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AAB24073 standard; Protein; 653

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29-JAN-2001

AAB24073;

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                                        44 AQTCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLE 103
                                                    ILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESI 163
                    71; Gaps
                                                                                                                                   HDLFTPLHHLERIHLHHNPWNCNCDILWLSWMIKDMAPSNTACCARCNTPPNLKGRYIGE
                                                                                                                                                                                                                                                          PSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDE
                                                                                                                                                                LDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLP
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 Length 713;
                      103; Indels
DB 22;
 Score 2131.5; DB 2;
Pred. No. 1.8e-145;
1; Mismatches 103;
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                     81;
  63.4%;
                      Conservative
            Similarity
            Local Simines 409;
  Query Match
                       Matches
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The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRO212, PRO390, PRO341, PRO335, PRO6199, PRO1037, PRO8039, PRO1059, PRO1009, PRO2199, PRO2199, PRO3197, PRO1111, PRO1153, PRO1009, PRO20094, PRO2199, PRO2199, PRO3197, PRO31710, PRO20094, PRO2199, PRO 20197, PRO1009, PRO20094, PRO2199, PRO 20197, PRO10097, PRO20094, PRO2199, PRO3199, PRO3197, PRO1009, PRO20094, PRO2199, PRO3199, PRO3197, PRO3190, PRO20094, PRO3190, PRO3
                                                            Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth; proliferation; tumour/genesis; identification; cancer; cytostatic; neuroprotective; antiinflammatory; immunosuppressive; immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; angiogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithalial disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immunologic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gurney AL, Hillan KJ,
                  Human PRO1111 protein sequence SEQ ID NO:46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 61; Fig 34; 286pp; English.
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99US-0141037.
99US-0143048.
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99WO-US30911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JAN-2000;
                                                                                                                                                                                                                                                                                                      Homo sapiens
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30-NOV-1999;
20-DEC-1999;
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07-JUL-1999;
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98US-0090461.
98US-0090472.
98US-0090535.
98US-0090538.
                                                      98US-0087607
98US-0087759
98US-0087759
98US-0088021
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98US-0089908.
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98US-0090688.
98US-0090690.
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                                                      02 - JUN - 1998;
02 - JUN - 1998;
03 - JUN - 1998;
04 - JUN - 1998;
05 - JUN - 1998;
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10-JUN-1998;
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16-JUN-1998;
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10-JUN-1998;
        09-DEC-1999
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                                                                                                                    14;
sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human PRO polynuclectide and protein sequences given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand; pharmaceutical; receptor immunoadhesin; gene mapping.
                                                                                                                                                                                            SVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGNTTASATLN 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLAMCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNA 262
                                                                                                                                                                                                                                                                                                                FDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNCDILWLSWWIKDMAPS 322
                                                                                                                                                                                                                                                                                                                                                                                                     NTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAELKCRASTSLT 382
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                                                                                                                                                                                                                                                AFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYL 202
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                                                                                                                     44; Gaps
                                                                                                                                            29 VLLALQLLVVAGLVRA-----QTCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLN 82
                                                                                                                                                            P--QSTRSTEKTFTIPVTDINSGI-PGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMR
                                                                                          Query Match 55.5%; Score 1865; DB 21; Length 653; Best Local Similarity 56.4%; Pred. No. 2.8e-126; Matches 363; Conservative 107; Mismatches 130; Indels 44
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                                                      653 AA;
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polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors. TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadheains, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially

by recombinant techniques.

653 AA;

Sequence

invention provides membrane-bound PRO polypeptides and

Membrane-bound proteins and related nucleotide sequences

WPI; 2000-072883/06

N-PSDB; AAZ65033

claim 12; Fig 157; 822pp; English

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Smith V, Watanabe CK;
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                                                              9805-0091478

9805-0091486

9805-0091628

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9805-0091633

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98US-0091358.
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98US-0091544.
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Yuan J;
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17-AUG-1998;
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11-AUG-1998;
11-AUG-1998;
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04-AUG-1998;
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04-AUG-1998;
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18-AUG-1998;
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26-AUG-1998;
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26-AUG-1998;
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26-AUG-1998
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16-SEP-1998
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Wood WI,
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                     Indels 44; Gaps
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                                                                                                                                                                                                                                22 vyltaqvwilcaaiaaaasagpqncpsvcscsnqfskvvctrrglsevpqgipsntryln
                                                                                    LHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNG
                                                                                                                                 143 AFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYL
                                                                                                                                             203 NLAMCNLREIPNETPLIKEDELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNA
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Length 653;
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Query Match 55.5%; Score 1865; DB 21; Best Local Similarity 56.4%; Pred. No. 2.8e-126; Matches 363; Conservative 107; Mismatches 130;
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                                                                                                                                                                                                                                                                                     Human; Alzheimer's disease; amyotrophic lateral sclerosis;
ALS; Zollinger-Ellison syndrome; immune system disease; schizophrenia;
inflammation, heematopoletic disease, anxiety; feeding disorder; aging;
anorexia; depression; cardiovascular disease; sleep disorder; seizure;
memory alteration; migraine; stroke; asthma; neuropathy; hypoglycaemia;
sexual disorder; growth abnormality; infection; autoimmune disease;
rheumatoid arthritis; cataractogenesis; angiogenesis; atherosclerosis;
cerebral ischaemia; cirrhosis; Huntington's disease; Hodgson's disease;
diabetes meallitus; glomerulonephritis; randiac arrhythmia; obesity;
diabetes meallitus; gene therapy; sbgPRO33ia gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New secreted and membrane associated polypeptides for treating Alzheimer's disease, psoriasis, cancer, enterocolitis, sleep and sexual disorders, stroke, and asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     They are also useful as vaccines for inducing an immunological response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a human sbgPRO331a protein, a membrane bound protein of the invention. The invention relates to secreted and membrane associated polypeptides
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                                                                           AAE09438 standard; Protein; 653 AA.
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2000US-0198583.
2000US-0237963.
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29-FEB-2000;
18-APR-2000;
04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:|| | :| | :| | :| | 493 vliqttr-vpkqvavpatdttdkmqtsldevmkttkiiigcfvavtllaaamlivfyklr
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in a mammal. Polynucleotides of the invention are used in gene They are also valuable for chromosome localisation studies and expression studies.
                                                                                                                                                                                44;
                                                                                                                                           Length 653;
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                                                                                                                                                                              Conservative 107; Mismatches
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                                                                                                                                                                 Similarity
                                                                                      653 AA;
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Matches
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ID AAU1
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14;

Gaps 82

44;

Length 653; Indels

Score 1865; DB 22; Pred. No. 2.8e-126;

55.5%; 56.4%;

Similarity

Query Match Best Local

Matches 363; Conservative 107; Mismatches 130;

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83 LHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNG 143 AFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYL

29 VLLALQLLVVAGLVRA-----QTCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLN

202

201

263 FDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNCDILWLSWWIKDMAPS

NLAMCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNA

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262 261 322 321 380 442

NTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAELKCRASTSLT 382

494 492

VTAA--TTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNV-----TTSLT

443

495 P--QSTRSTEKTFTIPVTDINSGI-PGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMR

|:| ::: |||||| ||::| | 552 krhggrstvtaartveligvdedipaatsaaataapsgvsgegavv]pti-hdhin-ynt

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601 YKSPFNHTTTVNTI-NSIH----SSVHEPLLIRMNSKDNVQETQI

552 KQHHRQNHHAPTRTVEIINVDDEITGDTPM-----ESHLPMPAIEHEHLNHYNS

SVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGNTTASATLN

W0200140466-A2

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99WO-US288301.
99WO-US28634.
99WO-US28551.
99WO-US28564.
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ME, Goddard A,
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                                                                                                                                                                                   (GETH ) GENENTECH INC
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                                                                                        06-JAN-2000;
11-FEB-2000;
18-FEB-2000;
18-FEB-2000;
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24-FEB-2000;
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                     01-DEC-2000;
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16-DEC-1999
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Gerritsen 1
                                                                                                                                                                                                        Smith V,
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ANUL2172-AAU12446 represent novel human secretory and transmembrane.

PRO polypeptides. The PRO polypeptides are useful to detect other

PRO polypeptides, to link bioactive molecules to cells expressing

PRO polypeptides, to modulate biological activities of cells expressing

PRO polypeptides, and to detect the presence of mammalian lung, colon,

breast, prostate, rectal, cervical or liver tumours by comparing PRO

Dolypeptide expression in a cell sample to that in a control sample.

Some of the 275 sequences are also useful to stimulate the release of

tumour necrosis factor-alpha (TNF-alpha) from human blood, the

proliferation or differentiation of chondrocytes, the proliferation or

gene expression in perioyte cells, the release of proteoglycans from

cartilage, the proliferation of inner ear utricular supporting cells or

of T-lymphocytes, the release of a cytckine from peripheral blood

monocytes (PBMCs), or the proliferation of endothellal cells. Some of

the PRO polypeptides may modulate glucose or free fatty acid uptake by

skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide

cof actor VIIA. The PRO polypeptides can be used in assays to identify

molecules involved in binding interactions. The polymuclecides encoding

PRO polypeptides can be used to generate probes, antisense RNA/NNA,

transgenic or knock out animals and can be used in gene therapy. 3 Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical Gao Deforge L, Desnoyers L, Filvaroff E, Ga A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang 2?. Claim 12; Fig 438; 813pp; English

Search completed: August 26, 2002, 15:40:58 Job time: 206 sec

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us-09-905-056-292.rpr

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Compugen Ltd.
GenCore version 4.5
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OM protein – protein search, using sw model

August 26, 2002, 15:39:27; Run on:

Search time 20.98 Seconds (without alignments) 2931.228 Million cell updates/sec

1 MLNKMTLHPQQIMIGPRFNR......VHEPLLIRMNSKDNVQETQI 640 US-09-905-056-292 3362 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283138 Total number of hits satisfying chosen parameters:

283138 segs, 96089334 residues

Searched:

length: 0 length: 2000000000 DB sed DB sed Minimum I Maximum I

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR_71:*

Database

pir1:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		hypothetical prote	glial cell membram	chondroadherin pre	neuronal leucine-r	slit-1 protein hom	MEGF5 protein - ra	slit protein 2 pre	М	īd		O	To.	insulin-like growt		insulin-like growt	insulin-like growt	insulin-like growt	decorin precursor	hypothetical prote	platelet glycoprot	decorin precursor	decorin precursor	decorin - rabbit	decorin precursor	G protein-coupled	lysine carboxypept	hypothetical profe	decorin precursor	oncofetal trophobl
ID	1 1	9	A58532	A53860	JC7763	T42218	T13953	B36665 .	A36665 .	T28714	T28715	T42626	S46224	JC5239	A60164	A41915	JC1282	JC6128	NBHUC8	T23841	NBHUIA	S24317	806280	147020	A55454	JG0193	A34901	T23836	S29145	A53531
n DB	!							7					2	2	2		3			7			2							
Length		4.2	109	361	707	1533	1523	146	148(78	135	102	153	90	26(9	603	9	326	294	62(35.	36(36(324	06	236	61(327	42(
Query Match		٠	12.4	12.2	12.1	11.9	11.1	10.4	10.4	10.4	10.4	10.2		-		•	9.3					•			•		9.8		8.5	
Score		13/0.5	411.5	410.5	406	399	374.5	350	350	348.5	348.5	344.5	337.5	332	329.5	320	312	311	302	296.5	296.5	293	293	293	290	289	287.5	287.5	287	286
Result No.	1	٦ (7	m	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

361

527

-	hypothetical prote	orphan G protein-c	gene wheeler prote	tlr protein - frui	hypothetical prote	hypothetical prote	biglycan precursor	proteoglycan I - m	biglycan precursor	biglycan precursor	hypothetical prote	hypothetical prote	hypothetical prote	chaoptin precursor	hypothetical prote	proline- arginine-
	T24315	JE0176	T13852	T13887	T25194	T19939	BGHUN	S20811	S32793	S32559	T19941	T15864	T34319	A29944	T29972	139068
	7	7	7	7	7	7	, ,	~1	7	7	~	~	~	Н	~	7
	603	907	1389	1385	653	680	368	369	369	369	458	1066	562	1134	575	382
	8.5	8.4	8.4	8.2	8.2	8.2	8.1	8.0	8.0	8.0	7.9	7.8	7.7	7.7	7.5	7.5
	286	283.5	281.5	276.5	275.5	275.5	271.5	27.0.5	270.5	269.5	264.5	262	258.5	257.5	252	250.5
	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

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477
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                                                                                                                                                                                                                                                                                                                                             266 LQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNCDILWLSWWIKDMAPSNTA 325
                                                                                                                                                                                                                                                                                                                                                                                             CCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAELKCRASTSLTSVS 385
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                        241 VDPVAAGGTGSGGGGGGGGGGGGGGGGTTYFTTVTVETLETQPGEEALQPRGTEKEPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                               386 WITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGNTTASATLNVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --ETTNVTTSLTPQSTRSTEKTFTIPVTDI-NSGIPGIDEVMKTT
                                                                                                                                                                                                                                         Length 421;
                                                                                                                                                                                                                                                                  58; Indels
                                                                                                  A.Reference number: 223034
A.Accession: T4626
A.Status: preliminary
A.Status: preliminary
A.Residues: 1-421 <AAA>
A.Cross_references: EMBL:AL137451
A.Stroperimental source: adult amygdala; clone DKF2p761A179
C.Genetics:
A.Note: DKF2p761A179.1
                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                        40.9%; Score 1376.5; DB 62.6%; Pred. No. 8.5e-83
Live 56; Mismatches 51
                                                                                                                                                                                                                                         Query Match
Best Local Similarity 62.69
Matches 256; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTPVVDW--
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us-09-905-056-292.rpr

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C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: JC7763
R;Fukamachi, K.; Matsuoka, Y.; Kitanaka, C.; Kuchino, Y.; Tsuda, H.
Biochem. Biophys. Res. Commun. 287, 257-263, 2001
                                                                                                                                                                                                                 507
                                                                                                                                                                            508 PVTDINSGIPGIDEVMKTTKII-IGCFVAITLMAAVMLVIFYKMRKQHHRQNHHAPTRTV 566
-- TPSLAVPLEDRVVTVGETVAFQCKATGSP 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 KRLSYISEGAFEGLSNLRYLNLAMCNLREIPN--LTPLIKLDELDLSGNHLSAIRPGSFQ
                                                                                                                  723 TPRITWLKGGRPLSLTERHHFTPGNQLLVVQNVMIDDAGRYTCEMSNPLGTERAHSQLSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 12.2%; Score 410.5; DB 2; Length Best Local Similarity 32.1%; Pred. No. 1.4e-19; Matches 111; Conservative 55; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 HNPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELD 345
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TAQNSAGSVSANATLTVLE---
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                                                          TPVVDWETTNVTTSLT-
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A; Residues: 1-1014 (2012)
A; Cross-references: GB:D78572; NID:g1545806; PIDN:BAA11416.1; PID:g1545807
A; Cross-references: GB:D78572; NID:g1545806; PIDN:BAA11416.1; PID:g1545807
C; Superfamily: leucine-rich alpha-2-glycoprotein repeat homology; cLRR1>
F; 36-61/Domain: proteoglycan amino-terferminal homology (LRR2>
F; 11-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology (LRR3>
F; 14-165/Domain: leucine-rich alpha-2-glycoprotein repeat homology (LRR3>
F; 191-213/Domain: leucine-rich alpha-2-glycoprotein repeat homology (LRR3>
F; 11-237/Domain: leucine-rich alpha-2-glycoprotein repeat homology (LRR5>
F; 21-237/Domain: leucine-rich alpha-2-glycoprotein repeat homology (LRR8>
F; 21-237/Domain: leucine-rich alpha-2-glycoprotein repeat homology (LRR9>
F; 26-285/Domain: leucine-rich alpha-2-glycoprotein repeat homology (LRR9>
F; 28-38-261/Domain: leucine-rich alpha-2-glycoprotein repeat homology (LR12>
F; 38-361/Domain: leucine-rich alpha-2-glycoprotein repeat homology (LR12>
F; 38-38-381/Domain: leucine-rich alpha-2-glycoprotein repeat homology (LR12>
F; 38-340/Domain: leucine-rich alpha-2-glycoprotein repeat homology (LR13>
F; 38-340/Domain: leucine-rich alpha-2-glycoprotein repeat hom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 LNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIP*140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----YAFNRIPSLRRLDLGELKRL-- 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            379 AFTGLDNLSKLTLFGNKIKSVAKRAFSGLESLEHLNLGENAIRSVQFDAFAKMKNLKELY 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAAELKCRASTSLT-SVSWITPNGTVMTHGAYKVRIAVLSDGTLNF-TNVTVQDTGMYTC 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDELDLSGNHLSAIRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         338 LRLSHNAISHIAEGAFKGLKSLRVLD-------LDHNEISGTIEDT--SG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.4%; Score 417.5; DB 2; Length 1091; 23.1%; Pred. No. 2.1e-19;
                                                                                      Species: Mus musculus (house mouse)
:Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change
                                                                                                                                                                      R;Suzuki, Y.; Sato, N.; Tohyama, M.; Wanaka, A.; Takagi, T. J. Biol. Chem. 271, 22522-22527, 1996
A;Title: CDNA cloning of a novel membrane glycoprotein that is A;Reference number: A58532; MUID:96394313
A;Accession: A58532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                          lial cell membrane glycoprotein LIG-1 precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87; Mismatches 208;
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                                                                                                                                                    Accession: A58532
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Matches 156;
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chondroadherin precursor - bovine
N;Alternate names: 38K leucine-rich protein
C;Species: Bos primigenius taurus (cattle)
C;Date: (07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 05-Nov-1999
C;Accession: A53860
R;Neame, P.J.; Sommarin, Y.; Boynton, R.E.; Heinegard, D.
J Blol. Chem. 269, 21547-21554, 1994
A;Title: The structure of a 38-KDa leucine-rich protein (chondroadherin) isolated fro A;Reference number: A53860; MUID:94342341
                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Rolecule type: mRNA
A; Rolecule type: mRNA
A; Cross-references: GB: U008018; NID: g470671; PIDN: AAA21330.1; PID: g470672
C; Superfamily: leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan carbox C; Keywords: disulfide bond
C; Keywords: disulfide bond
E; 300-346/Domain: proteoglycan carboxyl-terminal homology <PCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 VVLLALQLLVVAGLVRA-QTCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHEN 86
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A;Accession: T42218
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1531 <NAK>
A;Cross-references: EMBL:AB011530; NID:g3449289; PIDN:BAA32460.1; PID:g3449290
A;Cross-references: strain Sprague-Dawley; brain
C;Genetics: A;Gene: MEGF4
        A; Reference number: Z14126; MUID:98360089
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N;Alternate names: MEGF4 protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C;Accession: T42218
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
                                                                                A Accession: JC7763
A; Molecule type: mRNA
A; Molecule type: memba
A; Molecule type: memba
C; Comment: This protein, a new member of the neuronal leucine-rich repeat protein family in protein protein interaction and functions as a cell adhesion molecule or soluble light C; Genetics:
A; Gen
           gene
:Title: Rat neuronal leucine-rich repeat protein-3: Cloning and regulation of the Reference number: JC7763; PMID:11549284 contents: Fibrosarcoma cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----QIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWN 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LALQLLVVAGLVRAQTCPSVCSCS------NQFSKVICVRKNLREVPDGISTNTR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAITALVQAGDKKVD-CPQLCTCEIRPWFTPRSIYMEASTVDCNDLGLLNFPARLPADTQ 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLIKLDE-----LDLSGNHLSAIRPGSFQGLMHLQKLWM------IQS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 -PADLNVTEGMAAELKCRASTS-LTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 154;
                                                                                                                                                                                                                                                                                                                                                                                                     12.1%; Score 406; DB 2; Length 707;
Llarity 23.9%; Pred. No. 6.8e-19;
Conservative 98; Mismatches 239; Indels 1
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Best Local S:
Matches 154
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: T13953
C;Accession: M:: Nakajima, D:: Nagase, T:: Nomura, N:: Seki, N:: Ohara, O.
Genomics 51, 27-34, 1998
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                                                                                                                                                                                                                                                                                                                          SRLDLSENSLQAVPRKAFRGATDLKNLQLDKNQISCIEEGAFRALRGLEVLTLNNNNITT 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        || | | : :: | | :| | :| | :| | 376 VFGGLYTLQLLLLNANKINCIRPDAFQDLQNLSLLSLYDNKIQSLAKGTFTSLRAIQTLH 435
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                                                                                                                                              31 LALQLLVVAGLVRAQTCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQI 90
                                                                                                                                                                                                                18 LWLLLWAAAWRLGATACPALCTCTG - TTVDCHGTGLQAIPKNIPRNTERLELNGNNITR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 IPVSSFNHMPKLRTFRLHSNHLFCDCHLAWLSQWLRQRPTIGLFTQCSGPASLRGLNVAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :: || :| || :| || :| || :| || || || LELNGIKSIPPGAFSPYRKLRRIDLSNNQIAEIAPDAFQGLRSLNSLVLYGNKITDLPRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             393 -VMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGNTTASATLNVTAATTTPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     352 YAPVIVEPPADLNVTEGMAAELKCRASTSLTSVSWI----TPNGT------
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Query Match 11.9%; Score 399; DB 2; Length 1531; Best Local Similarity 22.7%; Pred. No. 5.4e-18; Matches 156; Conservative 101; Mismatches 235; Indels 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----LREIP--NLTPLIKLDELDLSGNHLSAIRPGSFQGLMH----
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Conservative
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109; Conserv
                               F;288-313/Domain:
F;323-346/Domain:
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Best Local S1
Matches 1099
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C;Genetics:
A/Gene: FlyBase:sI
C;Genetics:
A/Gene: FlyBase:sI
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A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs A;Reference number: Z14126; MUID:98360089 A;Accession: T13953
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(S.Specias: Drosophila melanogaster
(S.Specias: Drosophila melanogaster
(S.Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 19-May-2000
(S.Accession: B36665
(R.Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S. Genes Dev. 4, 2169-2187, 1990
(A.Title: Slit: an extracellular protein necessary for development of midline glia and A.Reference number: A36665; MUID: 91099665
                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                            A;Residues: Î-1523 <NAK>
A;Cross-references: EMBL:AB011531; NID:g3449291; PIDN:BAA32461.1; PID:g3449202
C;Genetics:
A;Gene: MEGF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 IKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKL 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 RILVTSFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLRQRRTIGQFTLCMAPVHLRGFSVA 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNL----
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Pred. No. 2.2e-16;
49; Mismatches 147; Indels 157;
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                                                                   A;Accession: T13953
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                            11.18;
25.48;
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Matches 120; Conservative
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A;Molecule type: mRNs
Residues: 1-1469 <ROT>
A;Cross-references: GB:X53959
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Best Local
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The protein 1 precursor - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 17-Nov-2000
C;Accession: A36665; A31640; S13523
R;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1999
A;Title: slit: an extracellular protein necessary for development of midline glia and A;Reference number: A36665; MUID:91099665
A;Status: preliminary
A;Molecule type: mRNA
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<LR12>
<LR13>
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F; 383-346/Domain: proceed1/gain amino-terminal incolology % PAMIX.
F; 347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology % LRRF F; 347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology % LRRF F; 395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology % LRRF F; 419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology % LRRF F; 450-494/Domain: proteoglycan carboxyl-terminal homology % PAMIX.
F; 512-537/Domain: proteoglycan amino-terminal homology % LRLF F; 557-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology % LRLF F; 557-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology % LRLF F; 561-695/Domain: proteoglycan carboxyl-terminal homology % LRLF F; 610-695/Domain: proteoglycan carboxyl-terminal homology % LRLF F; 610-695/Domain: proteoglycan amino-terminal homology % PAMIX.
F; 743-766/Domain: proteoglycan amino-terminal homology % LRLF F; 610-695/Domain: proteoglycan carboxyl-terminal homology % LRLF F; 610-695/Domain: Edge homology % EGFP.
F; 1008-10095/Domain: Edge homology % EGFP.
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<PAH2>
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us-09-905-056-292.rpr

Tue Aug

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A;Cross-references: EMBL:AF016687; PIDN:AAC48096.1; GSPDB:GN00022; CESP:T21D12.9a
A;Experimental source: strain Bristol N2; clone T21D12
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A;Introns: 38/2; 84/2; 132/2; 204/2; 275/2; 351/2; 519/3; 615/1; 714/1; 758/2
                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein T21D12.9a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T28714
R;Woessner, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  441 LNVTAATTTPFSYFSTVTVETM-----EPSQDEARTTDNNVGPTPVVDWETTNVTTSLTP 495
591 FEGASHIQELQLGENKIKEISNKMFLGLHQLKTLNLYDNQISCVMPGSFEHLNSLTSLNL 650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 SNTLAVCVEDGAVLYNTSMPFLRSLRFTNNQLRVIPKRAFERFPALEELDLTDNPIATIH
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                                                             299 HHNPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 NRLTTIPNGAFVYLSKLKELWLRNNPIESIP-----SYAFNRI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 GNHLS-AIRPGSF---QGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLP
                                                                                                 LDQNYFTCY - - - - APVIVEPPADLNVTEGMAAELKCRA - STSLTSVSW - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, August 1997
A;Description: The sequence of C. elegans cosmid T21D12.
A;Reference number: 220514
A;Reference number: 220514
A;Recession: T28714
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-789 < WWOE>
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                                                                                                                                                                                     359 PPADLNVTEGMAAELKCRASTSLTSVSWITPNGTVM 394
                                                                                                                                                                                                                                               ----ENSEGCLGDGYCPPSCTCT-----GTVV 726
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                                                                                                                                                                                                                                                                                                                                                                                                                    C; Keywords: 1321/3
C; Keywords: alternative splicing; growth factor
F; Mo-124/Domain: proteoglycan amino-terminal homology < LRR2>
F; 149-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR3>
F; Mo-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR5>
F; Mo-125/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR5>
F; Mo-137/Domain: proteoglycan carboxyl-terminal homology < RRR5>
F; Mo-137/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR8>
F; Mo-137/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR8>
F; Mo-134/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR9>
F; Mo-134/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR9>
F; Mo-137/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR9>
F; Mo-137/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR9>
F; Mo-137/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LR19>
F; Mo-137/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LR13>
F; Mo-137/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LR14>
F; Mo-137/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LR14>
F; Mo-
                                                                                                                    D. melanogaster involved in the development of
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<LR18>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  471 PIETSGARCESPKRMHRRRIESLREEKFKCSWGELRMKLSGECRMDSDCPAMCHCEGTTV 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------EIPNLTPL------IKLD------ELDLSGNHLSAIRPGS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DCTGRRLKEIPRDIPLHTTELLLNDNELGRISSDGLFGRLPHLVKLELKRNOLTGIEPNA 590
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                             PIDN:CAA37910.1; PID:98615
Z.; Artavanis-Tsakonas, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>
F;708-733/Domain: proteoglycan amino-terminal homology <PAH4>
F;743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology
F;767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology
F;791-814/Domain: leucine-rich alpha-2-glycoprotein repeat homology
F;815-838/Domain: leucine-rich alpha-2-glycoprotein repeat homology
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                                                                                                                                                                                                                                                  <R02>
                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 881-1182,'G',1185-1404,'GT',1463-1464,'YHA'
A;Cross-references: GB:M23543; NID:9340939; PID:9514357
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                   A,Cross-references: GB:X53959; NID:98614; R:Rothberg, J.M.; Hartley, D.A.; Walther, Gell 55, 1047-1059, 1988
A;Title: slit: An EGF-homologous locus of IA;Reference number: A31640; MUID:89077533
                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: FlyBase:FBgn0003425
A;Introns: 1351/3
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1068-1099/Domain: EGF homology <EGF2>
1115-1148/Domain: EGF homology <EGF1>
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19; Conservative
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F;1068-1099/Domain:
F;1115-1148/Domain:
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Matches 109;
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19;

89;

Length 789; Indels

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A/Title: Distinct but overlapping expression patterns of two vertebrate slit homologs A/Reference number: Z22177; MUID:99279238
A/Accession: T42626
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-1025 <HOL>
A/Cross-references: EMBL:AF074960; NID:94151258; PID:94151259; PIDN:AAD04345.1
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homology; proteoglycan amino-terminal hom
homology <PAH4>
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R. Nelson, R. E.; Fessler, L. I.; Takagi, Y.; Blumberg, B.; Keene, D.R.; Olson, P.F.;
EMBO J. 13, 3438-3447, 1994
A.; Title: Peroxidasin: a novel enzyme-matrix protein of Drosophila development.
A.; Reference number: S46224; MUID: 94341255
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C;Species: Drosophila sp.
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Oct-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 NFSNNKITDIEEGAFEGASGVNEILLTSNRLENVQHKMFKGLESLKTLMLKSNRISCVGN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 KGLKVLPKGIPKDVTELYLDGNQFTLVPKELSNYKHLTLIDLSNNRISTLSNQXFSNMTQ 298
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                                                                                                                                                                                                                                                                                                                                                                                                 47 CPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNS-FKHLRHLEIL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 QLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHNPWN 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 CNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLN 364
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                                                                                                                                                                                                                                                                                                                                                                                                                              2 CPEKCRCEG--TTVDCSNQRLNKIPDHIPQYTAELRLNNNEFTVLEATGIFKKLPQLRXI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 DSFIGLGSVRLLSLYD-NQITTVAPGAFDXLHSLSTLNLLANPFNCNCHLAWLGEWLRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 RIVTGNPRCQKPYFLKEIPIQDVAIQDFTCDDGNDDNSCSPLSRCPSECTCLDTXVRCSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLTLILSYNRLRCIPPRTFDGLKSLRLLSLHGNDISVVPEGAFNDLSALSHLAIGANPLY
                                                                                                                                                                                                                                                                                                                                                107;
                                                                                                                                                                                                                                                                                                Length 1025;
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Pred. No. 1.2e-14;
62; Mismatches 149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross_references: GB:U11052; NID:9531384; PIDN:1
C;Superfamilly: peroxidasin; myeloperoxidase homold
F:19-44/Domain: protecglycam amino-terminal homol
F;661-1350/Domain: myeloperoxidase homology 
                                                                                                                                                                                                                                                                                          10.2%;
24.3%;
                                                                                                                                                                                                                                                                                                                                                Conservative
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A; Residues: 1-1535 <NEL>
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Matches 106; Conserv
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                                                                                                                                                                                                                                                                                                                                                Matches 102;
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Best Local S
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R;Holmes, G.P.; Negus, K.; Burridge, L.; Raman, S.; Algar, E.; Yamada, T.; Little, M.H.
Mech. Dev. 79, 57-72, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 4
A;Introns: 38/2; 84/2; 132/2; 204/2; 275/2; 351/2; 519/3; 615/1; 714/1; 758/2; 786/3;
                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Mosidues 1.135 < WOED.
A; Residues: 1.135 < WOED.
A; Cross-references: EMBL.AF016687; PIDN: AAC48095.1; GSPDB:GN00022; CESP:T21D12.9b
A; Experimental source: strain Bristol N2; clone T21D12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                          hypothetical protein 721012.9b - Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        secreted leucine-rich repeat-containing protein SLIT2 - mouse (fragment)
N;Alternate names: neurogenic extracellular slit protein
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----ITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGNTTASAT 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : | || |:|: :: |:| || ||: || 340 PEAFEPL-ELKRLVMNSSSILCDCQISWLASWIYRLKLDKSSIIAKCSYPPPLADLYVVA 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDQNYFTCY----APVIVEPPADLNVTEGMAAELKCRA-STSLTSVSW------ 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNHLS-AIRPGSF---QGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLP 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         284 HDLFTPLHHLERIHLHHNPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGE 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            441 LNVTAATTTPFSYFSTVTVETM----EPSODEARTTDNNVGPTPVVDWETTNVTTSLTP 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --PSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPN--LTPLIKLDELDLS 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            496 OSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCF-----VAITLMAAVMLVIF 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 HTPKLKWLSL-HSNRIQSLPSGSFRVLRQLEELILSANSIDSLHKFALVGMSSLHKLDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                     submitted to the EMBL Data Library, August 1997
A;Description: The sequence of C. elegans cosmid T21D12.
A;Reference number: 220514
A;Accession: T28715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.4%; Score 348.5; DB 2;
llarity 24.3%; Pred. No. 9.5e-15;
Conservative 85; Mismatches 233;
                                                                                                                                                                                                                                                                                                                         Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 131; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene: CESP:T21D12.9b
                                                                                                                                                                       Accession: T28715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1
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Db 49	Qy 260 RNAFDNLQSLVEINLAHNNLTLLPHDLFTPL
RESULT 13 JG5239 Insulin-like growth factor acid-labile chain - baboon (Species: Papio sp. (baboon) (Species: Papio sp. (baboon) (Shacession: JG5239 (Shacession: JG5239 (Shacession: JG5239 (Shacession: JG5239) (Shacessi	A; Accession: A88030 A; Molecule type: DNA A; Residues: 1-560 <la2> A; Cross references: EMBL:233091; NID:g312501; PIDN:CAA80637.1; PID:g312502 A; Cross references: EMBL:233091; NID:g312501; PIDN:CAA80637.1; PID:g312502 A; Cross references: EMBL:233091; NID:g312501; PIDN:CAA80637.1; PID:g312502 A; Title: Rapid purification and characterization of human platelet glycoprotein V: th A; Reference number: A60164; MUID:90275263 A; Accession: A60164 A; Molecule type: protein A; Residues: 365-384 'X', 386-390, 'X', 397; 188-208, 'I', 210; 27-50, 'X', 52-53; I', X', 108, I', 51-72, 'Y', 'Y', 55-75, 'G', 479-487, 'X', 'A89-498, 'X', 500, 'X', 500, 'X', 500, 'X', 510, I', 1990 A; Title: Human platelet glycoprotein V: a surface leucine-rich glycoprotein related the A; Accession: A35483; MUID:90321220</la2>
Query Match 10.0%; Score 335; DB 2; Length 605; Best Local Similarity 20.8%; Pred. No. 2.5e-14; Atches 125; Conservative 64; Atches 125; Indels 286; Gaps 13; Qy 31 LALQLLVVA	A; Molecule type: protein A; Molecule type: protein A; Residues: 145-166, I', 168-169, X', 171-172 <rot> A; Residues: 145-166, I', 168-169, X', 171-172 <rot> A; Note: this proteolytic fragment was designated peptide M392 A; Molecule type: protein A; Residues: 121-129, W', 131-135, 466-468, X', 470 <ro2> A; Note: this material was designated peptide M393 but may contain two peptides A; Accession: C35483 A; Molecule type: protein A; Residues: 252-266, 'H', 268-272, 'X', 274-279, 'I', 281-284, 'I', 286 <ro3> A; Note: this proteolytic fragment was designated peptide M401 B; Zafar, R.S.; Walz, D.A.</ro3></ro2></rot></rot>
127	Trincomo. Ness. 35, 31-44, 1989 A; Tritle: Platelet membrane glycoprotein V: characterization of the thrombin-sensitive A; Reference number: A60432; MUID:8916231 A; Accession: A60432 A; Molecule type: protein A; Residues: 477-478, FX', 481-485, 'E', 487, 'V', 489-492,' NQ', 495, 'E', 497-498 <zaf> A; Residues: 477-478, FX', 481-485, 'E', 487, 'V', 489-492,' NQ', 495, 'E', 497-498 <zaf> R; Hickey, M.J.; Hagen, F.S.; Yaqi, M.; Roth, G.J. Proc. Natl. Acad. Sci. US; A. 90, 8327-8331, 1993 A; Title: Human platelet glycoprotein V: characterization of the polypeptide and the r A; Reference number: A47507 A; Reference number: A47507 A; Reterence number: A47507 A; Status: preliminary; translated from GB/EMBL/DBJ A; Molecule type: mRNA A; Status: preliminary; translated from GB/EMBL/DBJ A; Molecule type: mRNA A; Cross-references: GB:L11238; NID:g388759; PIDN:AAA03069.1; PID:g388760 C; Comment: This platelet membrane protein is a substrate for thrombin. C; Comment: The amino end of the intact protein is blocked. C; Comment: The amino end of the intact protein is syndrome. C; Genetics: A; Gene: GDB:GP5 A; Cross-references: GDB:230236; OMIM:173511</zaf></zaf>

104

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67 RLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALLGLENLCH 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLL 282
                                                         SYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPN--LTPLIKLD
                                                                                                                                                                                                                                                                                                                                                                                                              LOLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIP
                                                                                                                                            EVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEI-----
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Job time: 142 sec
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ol. Endocrinol. 6, 870-876, 1992
fittle: Structure and functional expression of the acid-labile subunit of the insulin-lacession: A41915; MUID:92357025
A;Map position: Spter-5qter
C;Superfamily: leucine-rich alpha-2-glycoprotein repeat homology
C;Keywords: blocked amino end; glycoprotein; platelet; tandem repeat; transmembrane prot
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                                                                                                                                                                                                                                                                                                                                                                                                                 ----LALHSNGLTALPDGLLRGLGKLRQVSLRRNRLRALPRALFRNLSSLESVQLDHNQ 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <LRR5>
<LRR6>
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                                                                                                                                                                                                                                                                                                       IKLDELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNN 278
                                                                                                                                                                                                                                                                                                                                                                                      LRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNN 158
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                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                  NLREVPDG------LHENQIQIIKVNSFKH 98
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A;Molecule type: mRNA; protein
A;Residues: 1-605 <LEO>
A;Cross-references: GB:M86826; NID:g184807; PIDN:AAA36047.1; PID:g184808
A;Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <LRR1>
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A Note: sequence extracted from NCBI backbone (NCBIP:110171)

C; Superfamily: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F; 75-99/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F; 99-122/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F; 99-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR F; 147-1194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR F; 171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR F; 195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR F; 195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR F; 219-226/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR F; 267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR F; 267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR F; 267-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR F; 313-318/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRI F; 318-318/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRI F; 318-318/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRI F; 318-318/Domain: leucine-ric
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Best Local Similarity 29.7%,
Matches 83; Conservative
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Gaps

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Conservative

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

August 26, 2002, 15:41:28; Search time 13.57 Seconds (without alignments) 1826.125 Million cell updates/sec Run on:

US-09-905-056-292 Title: Perfect score:

1 MLNKMTLHPQQIMIGPRFNR.....VHEPLLIRMNSKDNVQETQI 640 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	075325 homo sapien	bos t	008742 mus musculu	008770 rattus norv	-	002833 papio hamad		home	rattu	P70389 mus musculu	Homo	ednns	P07359 homo sapien	cani	Q9xsd9 sus scrofa .	P28675 gallus gall		Q28888 oryctolagus		P22792 homo sapien		Q9de66 coturnix co					-	O46403 equus cabal	P28653 mus musculu	P47853 rattus norv	O46390 ovis aries	Н	Q9z1s7 rattus norv
SUMMARIES	ID	GAC1_HUMAN	CHAD_BOVIN	GPV_MOUSE	GPV_RAT	SLIT_DROME	ALS_PAPHA	GPV_HUMAN	ALS_HUMAN	ALS_RAT	ALS_MOUSE	PGS2_HUMAN	PGS2_HORSE	GPBA_HUMAN	PGS2_CANFA	PGS2_PIG	PGS2_CHICK	PGS2_BOVIN	PGS2_RABIT	PGS2_MOUSE	CBP8_HUMAN	PGS2_RAT	KERA_COTJA	Y918_HUMAN	PLIB_AGKBL	KERA_CHICK	PGS1_HUMAN	PGS1_CANFA	PGS1_HORSE	PGS1_MOUSE	PGS1_RAT	PGS1_SHEEP	PGS1_BOVIN	OMD_RAT
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SM00082; LRRCT; 1. SM00013; LRRNT; 1. SM00369; LRR_TYP;

SMART; SMART; SMART;

	Q99mbl mus musculu										P23515 homo sapien
CHAO_TRICA	TLR3_MOUSE	CHAO_DROME	TLR7_HUMAN	Y848_HUMAN	PRLP_HUMAN	TLR3_HUMAN	TLR7_MOUSE	KERA_BOVIN	OMD_MOUSE	KERA_HUMAN	OMGP_HUMAN
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	258.5 7	256	254.5	253	250.5	249	249	248	247	246	245.5

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE Clial tumor;

MISSUB-Glial tumor;

MIDLINE-98324709; PubMed-9662332;

Malfoy B., Almeida A., Zhu X.X., Vogt N., Tyagi R., Muleris M.,

Dutrillaux A.-M., Dutrillaux B., Ross D., Hanash S.;

"GACI, a new member of the leucine-rich repeat superfamily on

GIROMOSOME band 1q32.1, is amplified and overexpressed in malignant
                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oncomer 16:2997-3002(1998).

-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

-!- TISSUE SPECIFICITY: OVERAMPLIFIED IN MALICANNY GLIOMAS.

-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

-!- SIMILARITY: CONTAINS 11 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                               16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Glioma amplified on chromosome 1 protein precursor.
                                                                                                    713 AA.
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InterPro; IPR001598; Ig_c2.
InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR_Cterm.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003592; LRR_out.
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Pfam; PF00560; LRR; 10.
Pfam; PF01462; LRRY; 1.
Pfam; PF01462; LRRYT; 1.
PRINTS; PR00019; LEURICHRPT.
SMART; SM00408; IGC2; 1.
SMART; SM00082; LRR; 6.
SMART; SM00082; LRRY; 1.
                                                                                                    STANDARD;
GAC1_HUMAN
ID GAC1_HUMAN
AC 075325;
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Immunoglobulin domain; Transmembrane; Glycoprotein; Repeat;
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                                                           GLIOMA AMPLIFIED ON CHROMO:
EXTRACELLULAR (POTENTIAL).
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EC8BC0FD240C9396 CRC64;
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LRR 11.
IG-LIKE C2-TYPE DOMAIN.
BY SIMILARITY.
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86; Mismatchés 228;
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Matches 147; Conservative
                      Leucine-rich repeat;
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                                                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. 270:431-436(1995).
                                                              Chondroadherin precursor (Cartilage leucine-rich protein) (38 kDa bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHONDROADHERIN, MINOR FORM.
10 X 24 AA LEUCINE-RICH TANDEM REPEATS.
                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                            Neame P.J., Sommarin Y., Boynton R.E., Heinegaard D.; "The Structure of a 38 *Rba leucine-rich protein (chondroadherin) isolated from bovine cartilage."; J. Biol. Chem. 269:21547-21554(1994).
                                                                                                                                                                                                                                                                                                              Hu B., Coulson L., Moyer B., Price P.A.; "Isolatrion and molecular cloning of a novel bone phosphoprotein related in sequence to the cystatin family of thiol protease inhibitors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 (IN SOME ISOFORM(S)).
                       (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHONDROADHERIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REF.
REF.
REF.
 361 AA.
                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
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InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR_Cterm.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003591; LRR_typ.
Pfam; PF00560; LRR: 10.
Pfam; PF001463; LRRCT; 1.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRCT; 1.
SMART; SM0013; LRRUT; 1.
REPEAT; SM00369; LRRUT; 1.
                                                                                                                                                                                                                                                                                              MEDLINE=95113864; PubMed=7814406;
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                                                                                                                                                                                      TISSUE-Cartilage;
MEDLINE-94342341; PubMed-8063792;
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 STANDARD;
                                                                                                    Bos taurus (Bovine).
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01-NOV-1997 (
30-MAY-2000 (
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CHAD_BOVIN
Q27972;
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Tue Aug 27 10:01:02 2002

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entities requires a license agreement (See http://www.isb-sib.ch/anhounce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                        | :: |||: || : ||| ORNNFPVLATNSFRAMPILVSLHLQHCQIREVAAGAFRGLKQLIYLYLSHNDIRVLRAGA 120
                                                                                                                                                                                                           SE-NSLSSLQPGALDDVENLAKFYLDRNQLSSYPSAALSKLRVVEELKLSHNPLKSIPDN<sub>4</sub> 239
                                                                                                                                        84 HENQIQIIKVNSFK-----HLRHLEI-------LQLSRNHIRTIEIGA 119
                                                                                                                                                                                          FNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDL 179
                                                                                                                                                                                                                                                                                              SFQGL-MHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERI 296
                                                                                                                                                                                                                                                                                                             GELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPN--LTPLIKLDELDLSGNHLSAIRPG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: THE GPIB-V-IX COMPLEX FUNCTIONS AS THE VON WILLEBRAND FACTOR RECEPTOR AND MEDIATES VON WILLEBRAND FACTOR-DEPENDENT BLOATELET ADHESION TO BLOOD VESSELS. THE ADHESION OF PLATELETS TO INJURED VASCULAR SURFACES IN THE APTERIAL CIRCULATION IS A CRITICAL INITIATING EVERY IN HEMOSTASIS (BY SIMILARITY). SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: CONTAINS 14 LEUCINE-RICH REPEATS (LRR).
                                                              37; Gaps
                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grunert P., Loew D., van Dorsselaer A., Cazenave J.-P., Lanza F.; "Gene cloning of rat and mouse platelet glycoprotein V: identification of megakaryocyte-specific promoters and demonstration blood 89:3253-3262(1997).
                                                                                       PLLVVLLALQLLVVAGLVRA-QTCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNL 83
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                      361;
                                                                                                                                                                                                                                                                                                                                                 345
                                                                                                                                                                                                                                                                                                                                                             STRAIN-C57BL/6; TISSUE-Liver;
MEDLINE-97275136; PubMed-9129030;
Ravanat C., Morales M., Azorsa D.O., Moog S., Schuhler S.,
Grunert P., Loew D., van Dorsselaer A., Cazenave J.-P., La
                                     Length
                                                                Indels
                                                                                                                                                                                                                                                                                                                                               HLHHNPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELD
DA79DC98AD3DD1F8 CRC64;
                                                             54; Mismatches 145;
                                     Score 411.5; DB 1;
Pred. No. 6.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Platelet glycoprotein V precursor (GPV) (CD42D).
                                                                                                                                                                                                                                                                                                                                                                                                                                      567 AA
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15-JUL-1998 (Rel. 36, Last seq
16-OCT-2001 (Rel. 40, Last ann
40884 MW;
                                    12.2%;
32.4%;
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                                                             Conservative
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361 AA;
                                                  Similarity
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                                                             Matches 113;
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008742;
SEQUENCE
                                    Query Match
                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 KLLDLSRNNLTHLPKGLLGAQVKLEKLLYSNQLTSVDSGLLSNLGALTELRLERNHLRS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 IEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                SMART; SM00370; LRR; 1.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_TPP; 10.
Platelet; Transmembrane; Glycoprotein; Blood coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
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C48643AA73967A7D CRC64;
                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                     PLATELET GLYCOPROTEIN V.
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                                                                                                                                                                                          Cell adhesion; Signal.
POTENTIAL.
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Pred. No. 8e-18;
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FAALPQLTQVLLGHNPWLCDCGLWRFLQWLRH------
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                           InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
Pfam; PF00560; LRR. 13.
Pfam; PF01463; LRRCT; 1.
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                LRR_Cterm.
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                                                                                                                                                                                       Repeat; Leucine-rich repeat; SIGNAL 16
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30.1%;
                                                                                                 PRINTS; PR00019; LEURICHRPT.
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IPR001611;
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567 AA;
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es 119; Conserv
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TRANSMEM
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Matches 121;
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P24014;
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REPEAT
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                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                              MENDANCE CONTRIBUTION FOR THE STATE OF THE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLATELET ADHESION TO BLOOD VESSELS. THE ADHESION OF PLATELETS TO INJURED VASCULAR SURFACES IN THE ARTERIAL CIRCULATION IS A CRITICAL INITIATING EVENT IN HEMOSTASIS (BY SIMILARITY).
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: CONTAINS 14 LEUGINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003592; LRR_out.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
Pfam; PF01463; LRRR; 14.
PRINTS, PR00019; LEURICHRPT.
SMART; SM00370; LRR; 2.
SWART; SM00082; LRRCT; 1.
SWART; SM00092; LRRCT; 1.
SWART; SM00099; LRRTyp; 10.
Platelet; Transmembrane; Glycoprotein; Blood coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell adhesion; Signal.
POTENTIAL.
PLATELET GLYCOPROTEIN V.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
LRR 1.
                                                                                                                                               15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Platelet glycoprotein V precursor (GPV) (CD42D).
----CRGP---EPRASLSFWELLQGDPWCPDPRSL 478
                                                                                                                                                                                                                                                                                                                             STRAIN-WISTAR; TISSUE-Liver;
MEDLINE-97275136; PubMed-9129030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRR
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InterPro; IPR0001611; LRR.
InterPro; IPR000483; LRR.Cterm.
InterPro; IPR000372; LRR_Nterm.
                                                                                                                             15-JUL-1998 (Rel. 36, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat; Leucine-rich repeat;
                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73
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TRANSMEM
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008770;
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451
                                                                       GPV_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219 IKLDELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNN 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTLLPHDLFTPLHHLERIHLHHNPWNCNCDILWLSWWI-----KDMAPSNTACCARC 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----KVICV-RKNLREVPDGI---STNTRLLNLHENQIQIIKVNSFKHLRHLE 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339 TELRVLAVHTNALEELPEDALRGLGRLRQVSLRHNRLRALPRTLFRNLSSLVTVQLEHNQ 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKTLPGDVFAALPOLTRVLLGHNPWLCDCGLWPFLQWLRHHLELLGRDEPP-----OC 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 ILDKMVL-LEQLFLDHNALRDLDQNLFQKLLNLR--------DLCLNQNQLSFL 161
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SE DEV. 4:2169-2187(1990).

FUNCTION: NECESSARY FOR DEVELOPMENT OF MIDLINE GLIA AND
COMMISSURAL AXON PATHWAYS. SLIT MAY INTERACT WITH EXTRACELLULAR
MATRIX MOLECULES.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rothberg J.M., Jacobs J.R., Goodman C.S., Artavanis-Tsakonas S.; "Slit: an extracellular protein necessary for development of midline glia and commissural axon pathways contains both EGF and LRR domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              452 NGPESRASLTFWELLQGDQWC--PSSRGLPPDPPTENALKAPDPTQRPNSSQSWAWV 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           331 NTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAELKCRASTSLTSVSWI 387
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MLNKMTLHPQQIMIGPRFNRALFDPLLVVLLALQLLVVAGLVRAQTCPSVCSCSNQFS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 PANLFSSLGKLKVLDLSRNNLTHLPQGLLGAQIKLEKLLYSNRLMSLDSGLLANLGALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPNLTP----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 PEVLFGEMAGLRELWLNG-THLRTLPAAAFRNLSGLQTLGLTRNPL--LSALPPGMFHGL
                                                                                                  (POTENTIAL).
                                                                                                                                                                          (GLCNAC. .) (POTENTIAL)
(GLCNAC. .) (POTENTIAL)
(GLCNAC. .) (POTENTIAL)
                                                                                                                                                        (POTENTIAL)
                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                     57;
                                                                                                                                                                                                                                                                                                                                   Length 567;
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                     LRR 13.
LRR 14.
LRR 14.
N-LINKED (GLCNAC...) (POT
W. CALO708E0D03707F CRC64;
                                                                                                                                                                                                                                                                                                                                10.8%; Score 361.5; DB 1; 29.0%; Pred. No. 2.8e-17; iive 59; Mismatches 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Slit protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1480 AA
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                                                                                                                                                                                                                                                          63344 MW;
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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LRR 19.
LRR 20.
LRR 21.
LRR 23.
LRR 24.
EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 2.
EGF-LIKE 5.
EGF-LIKE 5.
EGF-LIKE 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 || : || | | | : : : | |: : :: | | DAFRDLHSLSLLSLYD-NNIQSLANGTFDAMKSMKTVHLAKNPFICDCNLRWLADYLHKN 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 TCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEIL 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 YAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAM-----CNLR-----
                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL). (POTENTIAL). (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SING (IN SHORT ISOFORM). F9D5925FC170B1C3 CRC64;
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N-LINK
                                                                                                                                                                                                                       LAMININ G-LIKE.
EGF-LIKE 7.
CTCK.
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VARSPLIC
SEQUENCE
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                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collabotation between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- TISSUE SPECIFICITY: EXCRETED BY THE MIDLINE GLIA CELLS AND EVERTUALLY DISTRIBUTED ALONG THE AXONS.
-i- SIMILARITY: CONTAINS 7 EGF-LIKE DOMAINS.
-i- SIMILARITY: CONTAINS 24 LEUCINE-RICH REPEATS (LRR).
-i- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
-i- SIMILARITY: CONTAINS 1 LAMININ G-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00022; EGE_1; 7.
PROSITE; PS01186; EGE_2; 5.
PROSITE: PS01187; EGE_CA; 2.
PROSITE: PS50025; LAM_G_DOMAIN; 1.
PRUFOGENESIS; Glycoprotein; Signal; Alternative splicing; EGF-like domain; Repeat; Leucine-rich repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLIT PROTEIN
                                                                                                                                                                                                                                                                                                                                                   nost. Function 1978 FB90003425; sli.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000359; Cys_knot.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00010; ASX HYDROXYL; 3. PROSITE; PS01185; CTCK_1; 1. PROSITE; PS01225; CTCK_2; 1.
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LRR_Nterm.
LRR_out.
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Laminin_G
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EGF; 7.
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LRR; 17.
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EGF_CA; 2.
EGF_like; !
LRR; 4.
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LRRNT; 4.
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SMART; SM00179; E
SMART; SM00001; E
SMART; SM00370; L
SMART; SM0082; L
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SMART; SM00369;
SMART; SM00282;
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Pfam; PF01462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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                                                                                                                                                                                                                          FOGLMHLOKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHL 298
                                                                                                                                                                                                                                                                                                                               HHNPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVE 358
                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 41, Last annotation update)
1nsulin-like growth factor binding protein complex acid labile chain
IGFALS OR ALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Delhanty P., Baxter R.C.,
The cloning and expression of the baboon acid-labile subunit of the insulin-like growth factor binding protein complex.";
Blochem. Blophys. Res. Commun. 227:897-902(1996).
I- FUNCTION: INVOLVED IN PROTEIN-PROTEIN INTERACTIONS THAT RESULT IN PROTEIN COMPLEXES, RECEPTON-LIGAND BINDING OR CELL ADHESION.
I- SUBBUNIT: FORMA A TERMARY COMPLEX OF ABOUT 140 TO 150 kDa WITH IGF-ID A IGF-II AND IGFBP-3 (BY SIMILARITY).
I- SUBCELLULAR LOCATION: Extracellular.
I- SIMILARITY: CONTAINS 20 LEUGINE RICH REPEATS (LRR).
                                                                                                                          ------EIPNLTPL-----IKLD------ELDLSGNHLSAIRPGS
                                                                                                                                                             DCTGRRLKEIPRDIPLHTTELLLNDNELGRISSDGLFGRLPHLVKLELKRNQLTGIEPNA
                                                                       171 PIETSGARCESPKRMHRRRIESLREEKFKCSWGELRMKLSGECRMDSDCPAMCHCEGTTV
                                                                                                                                                                                                                                                                               FEGASHIQELQLGENKIKEISNKMFLGLHQLKTLNLYDNQISCVMPGSFEHLNSLTSLNL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Papio.

NCBI_TaxID=9557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----ENSEGCLGDGYCPPSCTCT-----GTVV 726
                                                                                                                                                                                                                                                                                                                                                                                                                                    PPADLNVTEGMAAELKCRASTSLTSVSWITPNGTVM 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  605 AA.
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HSSP; P23945; 1XUN.
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InterPro; IPR000483; LRR_Cterm.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
Pfam; PF00560; LRR; 19.
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SM00370; LRR; 2.
SM00082; LRRCT; 1.
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PF01462; LRRNT; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LALALLLISWVALGPRSLEGAEPGTPGEAEGPACPATCACSYDDEVNELS-VFCSSRNLT 66
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                       peat; Repeat; Signal.
BY SIMILARITY.
BROWLIN-LIKE GROWTH FACTOR BINDING
PROTEIN COMPLEX ACID LABILE CHAIN.
                                                                                                                                                                                                                                                                                                                                            ( ) (POTENTIAL) ( ) (POTENTIAL) ( ) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 605;
                                                                                                                                                                                                                                                                                                                                                                                                                10.0%; Score 335; DB 1; Length 60:
20.8%; Pred. No. 1.9e-15;
.ive 64; Mismatches 125; Indels
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                        Leucine-rich repeat;
                                                                       66110 MW;
         LRR_TYP; 11.
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SM00013; LRRNT; 1.
SM00369; LRR_TYP; 1
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580
605 AA;
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                        Glycoprotein;
SIGNAL
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CARBOHYD
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Usage by and for commercial
                              -- CNTPPNLKGRYIGELDQNYF 349.
487 LDVSHNRLEALPGSLLASLGRLRYLNLRNNSLRTFTPQPPGLERLWLEGNPWDCSCPLKA 5466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-94012616; PubMed-8407908; Lanza F., Morales M., de la Salle C., Cazenave J.-P., Clemetson K.J., Shimomura T., Phillips D.R., "Cloning and characterization of the gene encoding the human platelet 91ycoprotein V. A member of the leucine-rich glycoprotein V. A member of the leucine-rich glycoprotein family cleaved during thrombin-induced platelet activation."; J. Biol. Chem. 268:20801-20807(1993).
                                               | :| | | : | : :| : :| L----RDFALQNPSAVPRFVQAICEGDDCQPPVYTYNNITCASPPEVAGLDLRDLGEAHF 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 170:153-161(1990).
-!- FUNCTION: THE GPIB-V-IX COMPLEX FUNCTIONS AS THE VON WILLEBRAND FACTOR RECEPOR AND MEDIATES VON WILLEBRAND FACTOR-DEPENDENT PLATELET ABHESION TO BLOOD VESSELS. THE ADHESION OF PLATELETS TO INJURED VASCULAR SURFACES IN THE ARTERIAL CIRCULATION IS A CRITICAL INITIATING EVENT IN HEMOSTASIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-90321220; PubMed=2372284;
Roth G.J., Church T.A., McMullen B.A., Williams S.A.;
"Human platelet glycoprotein V: a surface leucine-rich glycoprotein
                                                                                                                                                                                                                                                                                                                                                     Hickey M.J., Hagen F.S., Yagi M., Roth G.J.; "Human platelet glycoprotein V: characterization of the polypeptide and the related Ib-V-IX receptor system of adhesive, leucine-rich
                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-90275263; PubMed-2350580;
Shimomura T., Fujimura K., Maehama S., Takemoto M., Oda K.,
Fujimoto T., Oyama R., Suzuki M., Icihara-Tanaka K., Titani K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Rapid purification and characterization of human platelet glycoprotein V: the amino acid sequence contains leucine-rich repetitive modules as in glycoprotein Ib."; Blood 75:2349-2356(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SIMILARITY: CONTAINS 14 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE Protein.
-1- TISSUE SPECIFICITY: PLATELETS AND MEGAKARYOCYTES.
-1- PTM: THE N-TERMINUS IS BLOCKED.
                                                                                                                                                                                                                                                                                                                                                                                                              roc. Natl. Acad. Sci. U.S.A. 90:8327-8331(1993)
                                                                                                                                                                          01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Platelet glycoprotein V precursor (GPV) (CD42D).
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MEDLINE-93391348; PubMed-7690959;
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01-FEB-1995 (Rel. 31, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                              LSWWIKDMAPSNTACCAR----
                                                                                                                                  STANDARD;
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                                                                                                                 GPV_HUMAN
ID GPV_HUMAN
AC P40197;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                           lycoprotein; Blood coagulation;
t; Cell adhesion; Signal.
POTENTIAL.
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(IN REF. 3).
PGG (IN REF.
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43; Mismatches
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               or send an email to license@isb-sib.ch)
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D -> W (
GID -> P
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                                                                                                                                  LRR_Nterm.
                                                                                                                    LRR_Cterm.
                                                                                                                                                           InterPro; IPR003591; LRR_typ.
Pfam; PF00560; LRR; 14.
Pfam; PF01463; LRRCT; 1.
                                                                                                                                                                                                       PRINTS; PRO0019; LEURICHRPT.
SMART; SM00370; LRR; 1.
SMART; SM00018; LRRUT; 1.
SMART; SM001013; LRRUT; 1.
SMART; SM00369; LRR TYP; 9.
Platelet; Transmembrane; Glyck
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                                                                                                                                 InterPro; IPR000372; LRR_Nter
InterPro; IPR003592; LRR_out.
                                                                                                                                                                                                                                                                                              Repeat; Leucine-rich repeat;
                                                        EMBL; 223091; CAA80637.1; -. HSSP; P16473; 1XUM.
MIM; 173511; -.
                                          EMBL; L11238; AAA03069.1;
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Best Local Similarity 29.7
Matches 83; Conservative
                                                                                                   InterPro; IPR001611; LRR
InterPro; IPR000483; LRR
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PRINTS; PRO0019; LEURICHRPT.
SMART; SMO0170; LRR; 2.
SMART; SMO0082; LRRCT; 1.
SMART; SM00013; LRRNT; 1.
SMART; SM0059; LRR_TYP; 1.
GLYCOPFOCE10; Leucine-rich repsignal
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Best Local Similarity 29.8
Matches 95; Conservative
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      ------ 343.
                                               219 IKLDELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNN 278
                                                                     01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 21, Last annotation update)
11sulin-11ke growth factor binding protein complex acid labile chain IGFALS OR ALS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baxter R.C., Martin J.L., Beniac V.A.; "High molecular weight insulin-like growth factor binding protein complex. Purification and properties of the acid-labile subunit from human serum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JUBER 1971. Chem. 264:11843-11848(1989).

-!- FUNCTION: INVOIVED IN PROPEIN-PROTEIN INTERACTIONS THAT RESULT
-!- FUNCTION: INVOIVED IN PROPEIN-PROTEIN INTERACTIONS THAT RESULT
IN PROTEIN COMPLEXES, RECEPTOR-LIGAND BINDING OR CELL ADHESION.
-!- SUBGINIT: FORMS A TERNARY COMPLEX OF ABOUT 140 TO 150 kDa WITH
IGF-I OR IGF-II AND IGFBP-3.
-!- SUBGELLULAR LOCATION: Extracellular.
-!- SINGELLULAR: CONTAINS 20 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Liver;
MEDLINE-92357025; PubMed-1379671;
Leong S.R., Baxter R.C., Camerato T., Dai J., Wood W.I.;
"Structure and functional expression of the acid-labile subunit the insulin-like growth factor-binding protein complex.";
Mol. Endocrinol. 6:870-876(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
301 QLRTLPAAAFRNLSRLRYLGVTLSPRLSALPQGAFQGLGELQV----
                                                                                                                                 279 LTLLPHDLFTPLHHLERIHLHNPWNCNCDILWLSWWIK 317
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
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MEDLINE=89308584; PubMed=2473065;
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InterPro; IPR003792; LRR_Nterm.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
Pfam; PF00560; LRR; 19.
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PIR; A41915, A41915.
HSSP; P23945; IXUN.
MIM; 601489; -.
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                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
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SEQUENCE FROM N.A.
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P35858;
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67 REPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFENLQGGQLGSLEPQALLGLENLCH 126
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                                                                                                     INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN.
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29.8%; Pred. No. 2e-14;
ive 50; Mismatches 124; Indels
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Leucine-rich repeat; Repeat; Signal.
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                                                              Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                 Dai J., Baxter R.C., "Molecular cloning of the acid-labile subunit of the rat insulin-like growth factor binding protein complex.";
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Insulin-like growth factor binding protein complex acid labile chain precursor (ALS).
                                                                                                                                                                                                                                              Purification and characterization of the acid-labile subunit of rat serum insulin-like growth factor binding protein complex."; Endocrinology 131:4846-852(1994).

-i- FUNCTION: MAY HAVE AN IMPORTANT ROLE IN REGULATING THE ACCESS OF CIRCULATING IGFS TO THE TISSUES.
-i- SUBUNIT: FORMS A TERNARY COMPLEX OF ABOUT 140 TO 150 kDa MITH IGF-I OR IGF-II AND IGFEP-3.
-i- SUBCELLULAR LOCATION: Extracellular.
-i- SUBCELLULAR LOCATION: Extracellular.
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                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 188:304-309(1992).
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MEDLINE-94130835; PubMed=7507839;
Baxter R.C., Dai J.;
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InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
Pfam; PF00560; LRR; 19.
Pfam; PF01463; LRRCT; 1.
Pfam; PF01462; LRRNT; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; JC1282; JC1282.
HSSP; P23945; IXUN.
InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR_
                                                                                                                   SEQUENCE FROM N.A.
                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52
74
98
121
121
169
1169
217
242
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SIGNAL
                                                     IGFALS OR ALS
                                                                                                                                 TISSUE-Liver
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70 VPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTL 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | ||| : | | : | | : | | : | 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NAR-2002 (Rel. 41, Last annotation update)
Insulin-like growth factor binding protein complex acid labile chain
precursor (ALS).
IGFALS OR ALS OR ALBS.
                                                                                                                                                                                                                                                                                                                                                                                                                                            67
                                                                                                                                                                                                                                                                                                                                                                                                              25 PLLVVLLALQLLV------VAGLVRAQTCPSVCSCSN----QFSKVICVRKNLRE 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-96413591; PubMed-8816745;
Bolsclair Y.R., Seto D., Haieh S., Hurst K.R., Ooi G.T.;
"Organization and chromosomal localization of the gene encoding the
mouse acid labile subunit of the insulin-like growth factor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                  225 DLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----EL----KRLSYISEGAFEGLSNLRYLNLAMCNLREIPN--LTPLIKLDEL
                                                                                                                                                                                                                            (GLCNAC. .) (POTENTIAL)
(GLCNAC. .) (POTENTIAL)
(GLCNAC. .) (POTENTIAL)
(GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                         9.3%; Score 312; DB 1; Length 603; 30.0%; Pred. No. 6.8e-14; ive 46; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                   LINKED (GLCNAC. . .) (P
DCD7637D94A5037C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 93:10028-10033(1996).
                                                                                                                                                                                               (GLCNAC.
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                             66811
                                                                                                                                                                                                                                                                                                                                                                             Conservative
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3312
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366
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                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=129/SV;
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P70389;
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EVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNT 128
                         cartilage. The II.";
                                                                           LELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYI
                                                                                                                                                 189 SEGAFEGLSNLRYLNLA-------MCNLREIPNLTPLIKLDELDLSGNHLSAIRPG
                                                                                                                                                                                      186 PDTVFQGLGNLHELVLAGNKLTYLQPALLCGLGE-----LRELDLSRNALRSVKAN
                                                                                                                                                                                                                           238 SFQGLMHLQKLWMIQSQIQVIERNAF------IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Danielson K.G., Fazina A., Cohen I.R., Cannizzaro L., Iozzo R.V. The human decorin gene: intron-exon organization, discovery of alternatively spliced exons in the 5' untranslated region, and mapping of the gene to chromosome 12q23."; Genomics 15:146-160(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-87017013; PubMed-3484330;
Krustus T., Ruoslahti E.;
Primary structure of an extracellular matrix proteoglycan core
protein deduced from cloned cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vetter U., Vogel W., Just W., Young M.F., Fisher L.W.; "Human decorin gene: intron-exon junctions and chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                               PGS2_HUMAN STANDARD; PRT; 359 AA. P07585; Q9Y5N9; Q9Y5N8; Q9P020; Q9P021; Q01-APR-1988 (Rel. 07, Created) Ol-APR-1988 (Rel. 07, Last sequence update) Ol-APR-2002 (Rel. 41, Last annotation update) Bone proteoglycan II precursor (PG-S2) (Decorin) (PG40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS A; B; C; D AND E).
Cs-Szabo G., Glant T.T.;
"Alternative splicing of human decorin.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roughley P.J., White R.J.;
"Dermatan sulphate proteoglycans of human articular oproperties of dermatan sulphate proteoglycans I and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=87250639; PubMed=3597437;
Fisher L.W., Hawkins G.R., Tuross N., Termine J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 83:7683-7687(1986).
                                                                                                                                                                                                                                                                                                                          274 LAHNNLTLLPHDLFTPLHHLERIHLHHN 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Lung;
MEDLINE-93162643; PubMed-8432527;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutherla; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                localization.";
Genomics 15:161-168(1993).
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FUNCTION: MAY HAVE AN IMPORTANT ROLE IN REGULATING THE ACCESS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 PLLVVLLALQLLV------VAGLVRAQTCPSVCSCS----NQFSKVICVRKNLR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CIRCULATING IGES TO THE TISSUES.
--- SUBUNIT: FORMS A TERNARY COMPLEX OF ABOUT 140 TO 150 kDa WITH IGF-I ON IGF-II AND IGFSP-3 (BY SIMMILARITY).
--- SUBCELLULAR LOCATION: Extracellular.
--- SIMILARITY: CONTAINS 21 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62;
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Pred. No. 8e-14;
4; Mismatches 122; Indels
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4A6223AEC7026BCC CRC64;
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SIMILARITY.
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(GLCNAC.
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LRR 20.
LRR 21.
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                                                                                                                                                                                                                                                                                           MGD; MGI:107973; Igfals.
InterPro; IPR001611; LRR.
InterPro; IPR0000483; LRR_Cterm.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003592; LRR_Out.
InterPro; IPR033591; LRR_typ.
Pfam; PF00560; LRR; 19.
Pfam; PF01462; LRRNI; 1.
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30.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00019; LEURICHRPT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00370; LRR; 4.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRNT; 1.
SMART; SMO0369; LRR_TYP;
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603 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; Connective tissue; Extracellular matrix; Proteoglycan; Repeat; Leucine-rich repeat; Signal; Alternative splicing;
                                                                                 -!- PTM: THE GLYCOSAMINOGLYCAN CHAIN ATTACHED TO DECORIN CAN BE EITHER CHONDROITIN SULFATE OR DERMATAN SULFATE DEPENDING UPON THE TISSUE OF ORIGIN.
-!- ALTERNATIVE PRODUCTS: 5 isoforms; A (shown here), B, C, D and E;
            "Purification and partial characterization of small proteoglycans I
                                                            RATE OF FIBRILS FORMATION. ALSO BINDS TO FIBRONECTIN AND TGF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
                                                                                                                                   are produced by alternative splicing. SIMILARITY: BELONGS TO THE SMALL INTERSTITIAL PROTEOGLYCANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GLYCOSAMINOGLYCAN)
                                                                                                                                                                      -1- SIMILARITY: CONTAINS 10 LEUCINE-RICH REPEATS (LRR).
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| L01125; AAA52301.1; JOINED.
| L01126; AAA52301.1; JOINED.
| L01127; AAA52301.1; JOINED.
| L01129; AAA52301.1; JOINED.
| L01130; AAA52301.1; JOINED.
| M98262; AAB60901.1; -
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PIR; S05640.
PIR; B28457; B28457.
PIR; A45016; A45016.
MIM; 125255;
InterPro; IPR001611; LRR.
InterPro; IPR00372; LRR_Nterm.
InterPro; IPR003591; LRR_LYP.
Pfam; PF01462; LRRR; 1.
SMART; SM00319; LRRR; 1.
SMART; SM00319; LRRR; 1.
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                                                                                                                                                                                                                                                                                             EMBL; M14219; AAB00774.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphism.
                                                                                                                                                             FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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15-JUL-1999 (Rel. 38, Last sequence update)
16-COT-2001 (Rel. 40, Last annotation update)
Bone protecoglycan II precursor (PG-S2) (Decorin) (Dermatan sulfate protecoglycan II) (DS-PGII)
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-!- FUNCTION: BILDS TO TYPE I AND TYPE II COLLAGEN AND AFFECTS THE RATE OF FIBRILS FORMATION. ALSO BINDS TO FIBRONECTIN AND TGF-BETA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 TFNGLNOMIVIELGTNPLKS-SGIENGAFOGMKKLSYIRIADTNITSIPQGLP-PSLTEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 AFNRIPSLRRLDLG--ELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDEL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Eguus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BETA (BY SIMILARITY).
PTM: THE GLYCOSAMINOGLYCAN CHAIN ATTACHED TO DECORIN CAN BE
CHONDROITIN SULFATE OR DERMATAN SULFATE DEPENDING UPON THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Richardson D.W., Dodge G.R.; "Effects of interleukin-1 beta and tumor necrosis factor-alpha expression of matrix related genes in cultured equine articular
                                                                                                                                                                                                                                                                                                                                                                        Query Match 9.0%; Score 302; DB 1; Length 359; Best Local Similarity 33.1%; Pred. No. 1.7e-13; Matches 85; Conservative 41; Mismatches 121; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE OF ORIGIN (BY SIMILARITY).
SIMILARITY: BELONGS TO THE SMALL INTERSTITIAL PROTEOGLYCANS
                                                                                        LDKV -> CLPS (IN ISOFORM E).
MISSING (IN ISOFORM E).
E -> Q (IN DBSNP:1803344).
/FTId-vAR_011975.
G -> A (IN REF. 6).
D -> P (IN REF. 6).
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                                                                                                                                                                                                                                                                                   FF511E871A1A52DD CRC64;
(IN ISOFORM B).
(IN ISOFORM C).
(IN ISOFORM D).
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                                                                                                                  Glycoprotein; Connective tissue; Extracellular matrix; Proteoglycan; Repeat; Leucine-rich repeat; Signal.
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(GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
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N-LINKED (GLCNAC. .) (POTENTIAL)
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BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                              (GLYCOSAMINOGLYCAN) (BY
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Pred. No. 2.7e-13;
47; Mismatches 150; Indels
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BONE PROTEOGLYCAN
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SIMILARITY)
           or send an email to license@isb-sib.ch)
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InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003592; LRR_out.
Pfam; PF00560; LRR: 9
Pfam; PG01462; LRRNT; 1.
SMART; SMO0370; LRR. 3.
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Matches 107; Conserv
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RESULT 13 GPBA_HUMAN

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MEDLINE-89025874; PubMed-2845978; Wenger R.H., Kieffer N., Wicki A.N., Clemetson K.J.; "Structure of the human blood platelet membrane glycoprotein Ib alpha
         01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Platelet glycoprotein IB alpha chain precursor (GP-IB alpha) (GPIBA)
GCD42B-alpha) (CC42B) [Contains: Glycocalicin].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT BSS VAL-172.
MEDIATE-938851, PubMed-7690774;
MEDIATE-9388851, PubMed-7690774;
WARTE J., RUSSELL S.R., MATCHESE P., MURATA M., MAZZUCATO M.,
de Marco L., Ruggeri Z.M.;
"Point mutathion in a leucine-rich repeat of platelet glycoprotein Ib
alpha resulting in the Bernard-Soulier syndrome.";
J. Clin. Invest. 92:1213-1220(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genetic and structural characterization of an amino acid dimorphism in glycoprotein Ib alpha involved in platelet transfusion refractoriness.";
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MEDLINE-87289655; Pubmed-3303030;
Lopez J.A., Chung D.W., Fujikawa K., Hagen F.S., Papayannopoulou T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT BSS SER-225.
MEDILINE-95118882; Pubmed-7819107;
Simsek S., Noris P., Lozano M., Pico M., von Dem Borne A.E.G.K.,
Ribera A., Gallardo D.;
"Cys209 Ser mutation in the platelet membrane glycoprotein Ib alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1/-31.
MEDLINE-87398554; PubMed-3497398; AILTHO-87399554; Titani K., Takio K., Handa M., Ruggeri Z.M.; Titani K., Takio K., Handa M., Ruggeri Z.M.; Amino acid sequence of the von Willebrand factor-binding domain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-92110577; PubMed=1730088; Miller J.L., Lyle V.A., Cunningham D.; Multation of leucine-57 to phenylalanine in a platelet glycoprotein Ib alpha leucine tandem repeat occurring in patients with an autosomal dominant variant of Bernard-Souller disease."; Blood 79:439-446(1992).
                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                     "Cloning of the alpha chain of human platelet glycoprotein Ib: a transmembrane protein with homology to leucine-rich alpha 2-glycoprotein,";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-91301149; PubMed-2070794;
Hess D., Schaller J., Rickli E.E., Clemetson K.J.;
"Identification of the disulphide bonds in human platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-92265982; PubMed-1586750;
Murata M., Furihata K., Ishida F., Russell S.R., Ware J.,
                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 84:5615-5619(1987).
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Proc. Natl. Acad. Sci. U.S.A. 84:5610-5614(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blood 79:3086-3090(1992).
                                                                                                                                                   Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-95178321; PubMed-7873390;
MEDLINE-95178321; PubMed-7873390;
A del a Salle C., Baas M.-J., Lanza F., Cazenave J.-P.;
A chevalier J., Gachet C., Briquel M.-E., Cazenave J.-P.;
Thereat of platelet glycoprotein Ib alpha associated with a variant of Bernard-Soulier syndrome (Nancy I).";
Br. J. Haematol. 89:386-396(1995).
-I- FUNCTION: GP-IB, A SURFACE MEMBRANE PROTEIN OF PLATELETS,
PARTICIPATES IN THE FORMATION OF PLATELET PLOGS BY BINDING TO VON WILLEBRAND FACTOR, WHICH IS ALREADY BOUND TO THE SUBENDOTHELIUM.
C. -I- SUBUNIT: GP-IB ALPHA AND BETA ARE DISULFIDE LINKED. GP-IX IS
C. OMPLEXED WITH THE GP-IB HETERODIMER VIA A NON COVALENT LINKAGE.
C. -I- SUBCLIULAR LOCATION: Type I membrane protein.
C. -I- THE GLYCOCALICIN, WHICH IS APPROXIMATELY COEXTENT LINKAGE.
C. -I- PTM: GLYCOCALICIN, WHICH IS APPROXIMATELY COEXTENT HTHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLYMORPHISM: POSITION 161 IS ASSOCIATED WITH PLATELET-SPECIFIC . ALLOAWTISEN SIBA. SIBA(-) HAS THR-161 AND SINA(+) HAS MET-161 SIBA IS INVOLVED IN NEONATAL ALLOIMUNE THROMBOCYTOPENIA (NATP). DISEASE: DEFECTS IN GPIBA ARE ONE OF THE CAUSES OF BENARD-SOULIER SYNDROME (BSS). BSS PATIENTS HAVE UNUSUALLY LARGE PLATELETS AND HAVE A CLINICAL BLEEDING TENDENCY. DISEASE: DEFECTS IN GPIBA ARE ONE OF THE CAUSES OF VON WILLEBRAND DISEASE (VWD) KNOWN AS PLATELET-TYPE VON WILLEBRAND DISEASE OR
                                                                                                                                                                                                                                                                                         MEDLINE-93253059; PubMed-8486780; Murata M., Russell S.R., Ruggeri Z.M., Ware J.; Expression of the phenotypic abnormality of platelet-type von Willebrand disease in a recombinant glycoprotein Ib alpha fragment."; J. Clin. Invest. 91:2133-2137(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF WWF FROM THE CIRCULATION.
MISCELLANBOUS: PLATELET ACTIVATION APPARENTLY INVOLVES DISRUPTION
OF THE MACROMOLECULAR COMPLEX OF GP-IB WITH THE PLATELET
OF THE MACROMOLECULAR COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSEUDO-VON WILLEBRAND DISEASE. THIS AUTOSOMAL DOMINANT BLEEDING DISORDER IS CAUSED BY AN INCREASED AFFINITY OF GP-IB FOR SOLUBLE VWF RESULTING IN IMPAIRED HEMOSTATIC FUNCTION DUE TO THE REMOVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Pseudo-von Willebrand disease: a mutation in the platelet
glycoprotein Ib alpha gene associated with a hyperactive surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISCELLANDONS: BINDING SITES FOR VON WILLEBRAND FACTOR AND THROMBIN (THE LATTER SITE WITH UNKNOWN FUNCTION) ARE IN THE AMINO-TERMINAL PART OF THE MOLECULE.
SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF THE MACROMOLECULAR COMPLEX OF GP-IB WITH THE PLATELEY GLYCOPROTEIN IX (GP-IX) AND DISSOCIATION OF GP-IB FROM THE ACTIN-BINDING PROTEIN.
                                                                                                      MEDLINE-91271273; PubMed-2052556;
Miller J.L., Cunningham D., Lyle V.A., Finch C.N.;
Mutation in the gene encoding the alpha chain of platelet
glycoprotein Ib in platelet-type von Willebrand disease.";
Proc. Natl. Acad. Sci. U.S.A. 88:4761-4765(1991).
gene is associated with Bernard-Soulier syndrome.";
Br. J. Haematol. 88:839-844(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93214031; PubMed=8384898; Russell S.D., Roth G.J.;
                                                                                                                                                                                                                                                                     VARIANT PSEUDO-VWD VAL-249.
                                                                               VARIANT PSEUDO-VWD VAL-249
                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT PSEUDO-VWD VAL-255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DURING PLATELET LYSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blood 81:1787-1791(1993).
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SMART; SM00082; LRRCT; 1.
SMART; SM0013; LRRWT; 1.
SMART; SM00369; LRR_TXP; 1.
Platelet; Transmembrane; Glycoprotein; Hemostasis; Blood coagulation;
                                                                                                                                                                                                                                                      Repeat; Leucine-rich repeat; Signal; Cell adhesion; Disease mutation; Polymorphism; von Willebrand disease; Bernard Soulier syndrome. SIGNAL 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 NTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DTTILHLSENLLYTFSLATLMPYTRLTQLNLDRCELTKLQVD--GTLPVLGTLDLSHNQL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 TTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNLRYLNLAMCNLREIPN--LTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQ 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 PLLVVLLALQLLVVAGLVRAQTCPS-----VCSCSNQFS--KVICVRKNLREVPDGIST 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLYCOPROTEIN IB ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 193; Indels 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTIG=VAR_005256.
T -> M (IN ALLOANTIGEN SIBA(+)).
/FTIG=VAR_005257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 626;
                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R -> H (IN DBSNP:6068).
/FTId=VAR_011909.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
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N-LINKED (GLCNAC.
O-LINKED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISSING (IN BSS).
/FTId=VAR_005259.
C -> S (IN BSS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VAR_005258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 8e-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L -> F (IN BSS)
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THR/PRO-RICH
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LRR 2.
LRR 3.
LRR 4.
LRR 5.
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                                                                       LRR_Cterm.
LRR_Nterm.
                                                                                                 InterPro; IPR003592; LRR_out.
                                                                                                                LRR_typ.
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SMART; SM00370; LRR; 3.
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                                                                                                                                         LRRCT; 1.
                                                           InterPro; IPR001611; LRR
                                                                                                                InterPro; IPR003591; LF
Pfam; PF00560; LRR; 6.
Pfam; PF01463; LRRCT; 1
Pfam; PF01462; LRRNT; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                              210
386
395
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417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161
PIR; A27075; NBHUIA.
GlycoSuiteDB; P07359;
                                                                        InterPro; IPR000483;
InterPro; IPR000372;
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EMBL; J02940; AAA52595.1; -. EMBL; M22403; AAA52596.1; -.

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FTC 351
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               InterPro;
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DISULFID
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           255 IQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNCDILWLSW 314
140 GELQELYLKGNELKTLPPGLLTPTPKLEKLSLANNNLTELPAGLLNGL------ 187
                                                                                                                                                     392 TVMTHGAYKVRIAVLSDGTLNFT----NVTVQDTGMYTCMVSNSVGNTTAS------438
                                                                                                                                                                                342 LHPTQESTKEQTTFPPRWTPNFTLHMESITFSKTPKSTTEPTPS--PTTSEPVPEPAPNM 399
                                                                                                                                                                                                                    -----ENLDTLL---LQENSLYTIPKGFFGS-HLLPFAFLHGNPWLCNCEILYFRR 234
                                                                   WIKDMA------ELDQNYFTC 351
                                                                                       235 WLQDNAENVYVWKQGVDVKAMTSNVASVQCDNSDKFPVYKYPGKGCPTLGDEGDTDLXDY 294
                                                                                                              YAPVIVEPPADLNVTEGMAAELKCRASTSLTS------VSWIT-----PNG 391
                                                                                                                                   Y-----PEED---TEGD----KVRATRTVVKFPTKAHTTPWGLFYSWSTASLDSQMPSS 341
                                                                                                                                                                                                     ATLNVTAATTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETT-----NVTTSL 493
                                                                                                                                                                                                                                                494 TPQSTRSTEKTFTIPVTDINS---GIPGIDEVMKTTKIIIG--------CFV 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 10 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                16-CCT-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Bone proteoglycan II precursor (PG-S2) (Decorin).
DCN OR DCNIC.
                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                          535 AI-----TLMAAVMLVI 546
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504 PLGFYVLGLFWLLFASVVLIL 524
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15-JUL-1998 (Rel. 36, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 244-259 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U83141; AAB51245.1; -. EMBL; L77684; AAA98062.1; -. InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Q29393;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 PLLKLERLYLSKNHLKELPE---KMPKTLQELRAHENEITKVRKAVFNGLNOMIVVELGT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 NN--NISA-----VGSNDFCPPGYNTK---KASYSGVSLFSNPVQYWEIQPST 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                         Extracellular matrix; Proteoglycan;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPRFNRALFDPLL------VVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 GPFQQRGLFDFMLEDEASGIGPEDRAPDMPDLELL-----GPVCPFRCQC--HLRVVO 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 -ELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 GLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLG-
                                                                                                                                                                                                                                                                                                                                                                                                                     . .) (POTENTIAL). . .) (POTENTIAL). . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                        (GLYCOSAMINOGLYCAN) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 295; DB 1; Length 36(; Pred. No. 5e-13; 45; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99BEE11A9C812906 CRC64;
                                                                                                                                                                            BY SIMILARITY.
BONE PROTEOGLYCAN II.
                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
N-LINKED (GLCNAC..
N-LINKED (GLCNAC..
N-LINKED (GLCNAC..
SY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                           Signal.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                         O-LINKED
              InterPro; IPR003591; LRR_typ.
Pfam; PR00569; LRR; 9.
Pfam; PF01462; LRRH; 1.
SMART; SM00370; LRR; 2.
SMART; SM00013; LRRNT; 1.
GNART; SM0369; LRR TYP; 1.
GlycoproteIn; Connective tissue; Ex
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LERR 2.
LERR 3.
LERR 5.
LERR 6.
LERR 7.
LERR 9.
LERR 9.
LRR_out.
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                                                                                                                                         Repeat; Leucine-rich repeat;
SIGNAL 16
PROPEP 17 30
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Matches 106; Conservative
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                                                                                                                         -
                                                                                                                                                                                                                                         BETA (BY SIMILARITY).
-!- PTM: THE GLYCOSAMINOGLYCAN CHAIN ATTACHED TO DECORIN CAN BE EITHER CHONDROITIN SULFATE OR DERMATAN SULFATE DEPENDING UPON THE TISSUE OF ORIGIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRR 10.
O'LINKED (GLYCOSAMINOGLYCAN) (BY
SIMILARITY).
N'LINKED (GLCNAC. .) (POTENTIAL).
N'LINKED (GLCNAC. .) (POTENTIAL).
BY SIMILARITY.
POTENTIAL.
                                                                                                                                                                  STRAIN-YORKSHIRE; TISSUE-AOTE;
Stephenson S., Schnoke M., Vesely I.;
"Alternatively spliced version of the porcine decorin gene.";
"Alternatively spliced version of the BMB/GenBank/DDBJ databases.
Submitted (APR-1999) to the BMB/GenBank/DDBJ databases.
-i- FUNCTION: BINDS TO TYPE I AND TYPE II COLLAGEN AND AFFECTS THE RATE OF FIBRILS FORMATION. ALSO BINDS TO FIBRONECTIN AND TGF-
                     Sus scrofa (P1g).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID-9823,
                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE SMALL INTERSTITIAL PROTEOGLYCANS
                                                                                                      Stephenson S., Schnoke M., Vesely I.; "Cloning of the porcine decorin gene."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISSING (IN SHORT ISOFORM).
8573DE8DDEBA7509 CRC64;
                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 10 LEUCINE-RICH REPEATS (LRR).
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BONE PROTEOGLYCAN II.
Bone proteoglycan II precursor (PG-S2) (Decorin)
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                                                                                                                                                        SEQUENCE FROM N.A. (SHORT FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003592; LRR_out.
                                                                                 SEQUENCE FROM N.A. (LONG FORM).
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  285 DLFTPLHHLERIHLHHNPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIG-- 342
                                                                                                        47 CPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQ 106
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                                                         Gaps
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                                                      38;
8.8%; Score 295; DB 1; Length 360; 30.5%; Pred. No. 5e-13; Live 44; Mismatches 139; Indels
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                                                    Conservative
                           Similarity
                                                    97;
Query Match
Best Local S:
Matches 97,
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Search completed: August 26, 2002, 15:45:35 Job time: 247 sec

09cyk3 mus musculu 06cH809 mus musculu 06cH809 mus musculu 09cH809 homo sapien 09byB8 homo sapien 09cfj5 homo sapien 09cfj5 mus musculu 09cfj5 mus musculu

P70193 mus musculu 015335 homo sapien Q9esy6 rattus norv

Q9nzul homo sapien Q9wvb5 mus musculu O94898 homo sapien

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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SEQUENCE FROM N.A.
MEDLINE=20450683; PubMed=10997877;
Magase T., Kikuno R., Nakayama M., Ohara O.;
Magase T., Kikuno R., Nakayama M., Hirosawa M., Ohara O.;
Prediction of the coding sequences of unidentified human genes.
XVIII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA RES. 7:273-281(2000).
EMBL: AB046800; BAB13406.1;
HSSP; P22888; ILUT.
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Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
KIAALSB0 PROTEIN (FRAGMENT).
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Q9WVB5
Q9WVB5
Q98Z98
Q88Z70
Q95Z10
Q9Z6Z6
Q5Z2Z6
Q9Z6Z6
Q9ZZZ6
Q9ZZQ6
Q9ZQ6
Q9P231
073675
Q9CYK3
Q61809
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Q9BYB8
P97860
Q96RJ5
P70193
O15335
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Q9NZU0
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InterPro; IPR003599; 19.
InterPro; IPR003609; 19_16.
InterPro; IPR003000; 19_11ke.
InterPro; IPR003000; 19_MHC.
InterPro; IPR000483; IER_Cterm.
InterPro; IPR000483; IER_Cterm.
InterPro; IPR000372; IER_NETERM.
InterPro; IPR003591; IER_VETERM.
Pr00047; 19; 1.
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       Homo sapiens (Human).
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Q96fe5 homo sapien
Q96fe5 homo sapien
Q90008 macaca fasc
Q9dlt0 mus musculu
Q9bz20 homo sapien
Q96ni6 homo sapien
Q9430 drosophila
Q94410 homo sapien
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3235.440 Million cell updates/sec
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Q9hbwl homo sapien
Q96a85 homo sapien
Q9nt99 homo sapien
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                                                                                                                                                                                                                                                                                                                               640
                                                                                                                                                                              Search time 34.22 Seconds
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1 MLNKMTLHPQQIMIGPRFNR.....VHEPLLIRMNSKDNVQETQI
                            GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      562222 seqs, 172994929 residues
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                                                                                                                                                                           August 26, 2002, 15:41:03;
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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096A85
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099PH1
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09N008
09BZZO
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096NIG
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Gapop 10.0 , Gapext 0.5
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sp_human:*
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sp_mammal:*
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Pfam; PF01463; LRRCT; 1.
Pfam; PF01463; LRRVT; 1.
PRINTS; PR00019; LEURICHRPT.
SMART; SM00409; IG; 1.
SMART; SM00408; IGC2; 1.

09be71 macaca fasc 043377 homo sapien 09h3w5 homo sapien 099kt6 mus musculu

Q9BE71 O43377 Q9H3W5 Q99KT6

Result õ homo sapien macaca fasc

088279 rattus norv 095710 homo sapien 095810 homo sapien 095826 mus musculu 095527 homo sapien 0957109 mus musculu 097109 mus musculu 097109 mus musculu 097010 rattus norv 070210 rattus norv 09083 xenopus lae

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                                                                                                      1 MLNKMTLHPQQIMIGPRFNRALFDPLLVVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKV 60
                                                                                                             NPWNCNCDILMLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPP
                                                                                                                                                                                                                                                                                                                                       ELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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0
                                                                          640;
                                                                         Length
                                                                                         Indels
                                                    6058974872636838 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ol-Our-2001 (TrEMBLrel. 18, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) MARIN TUMOR ASSOCIATED PROTEIN NAG14.
                                                                                                                                                                                                                                                                                                                                                                                                Score 3362; DB 4;
Pred. No. 2.3e-240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    653 AA
                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                                       ö
                                                   640 AA; 71949 MW;
                                                                         100.0%;
ilarity 100.0%;
Conservative 0
SMART; SM00410; IG_like; 1.
SMART; SM00370; LRR; 6.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                      Immunoglobulin domain.
                                                                                 Similarity
                                                                                       Matches 640;
                                             NON_TER
SEQUENCE
                                                                         Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NLAMCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   443 VTAA--TTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNV-----TTSLT 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P--QSTRSTEKTFTIPVTDINSGI-PGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMR 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 VYLTAQVWILCAAIAAAASAGPQNCPSVCSCSNQFSKVVCTRRGLSEVPQGIPSNTRYLN
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                                                                                                                                             Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
J., Bin L., Jiang N., Li G.; sapiens brain-specific gene (BAG), downregulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_TYP; 7.
Immunoglobulin domain.
SEQUENCE 653 AA; 72717 MW; 38159C81F6850E37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 55.5%; Score 1865; DB 4;
Best Local Similarity 56.4%; Pred. No. 1.2e-129;
Matches 363; Conservative 107; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001611, LRR.
InterPro; IPR001611, LRR.
InterPro; IPR001611, LRR.
InterPro; IPR001612, LRR.Cterm.
InterPro; IPR00152, LRR.Nterm.
InterPro; IPR001591, LRR.Ltyp.
InterPro; IPR001591, LRR.Ltyp.
InterPro; IPR001591, LRR.Ltyp.
IPfam; PF001461, LRR; 8.
IPfam; PF001462; LRR; 8.
IPfam; PF001462; LRR; 1.
INTERPRO; INTERPR
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Interpro; IPR003598; Ig.c2.
Interpro; IPR003600; Ig_like.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR001611; IRR.
                                                                                                                                                                                    EMBL; AF196976; AAG28019.2;
HSSP; P23945; 1XUN.
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 AFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYL #202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLAMCNIREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNCDILWLSWWIKDMAPS 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 VLLALQLLVVAGLVRA-----QTCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLN 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAELKCRASTSLT
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552 KRHQQRSTVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEGAVVLPTI-HDHIN-YNT
                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang J.;
Thesis (2000), Zhongshan Medical University, Guangzhou, China.
EMBL; AJ297858; CAC82651.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 72.3 KDA PROTEIN.
                                     601 YKSPFNHTTTVNTI-NSIH---SSVHEPLLIRMNSKDNVQETQI
                                                               11arity 56.1%; Score 1840; DB 4; 56.1%; Pred. No. 8.7e-128; Conservative 105; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
9C11C5ABC7E536CF
                                                                                                                                                                                 649 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal Hypothetical protein.
SIGNAL 1 38 PC
SEQUENCE 649 AA; 72313 MW;
                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                            (Human)
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Best Local Similarity
Matches 361; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                            Homo sapiens
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445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 MCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDN 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----FSYFSTVTVETME--PSQD--EARTTDNN-VG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---ETTNVTTSLTPQSTRSTEKTFTIPVTDI-NSGIPGIDEVMKTT 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     266 LQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNCDILWLSWWIKDMAPSNTA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blum H., Bauersachs S., Mewes H.W., Gassenhuber J., Wiemann S.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.9%; Score 1376.5; DB 4; Length
62.6%; Pred. No. 9.2e-94;
.ive 56; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164C6AF1A4BC440C CRC64;
                            :=::= = = ::: :: :: ::
                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 45.1 KDA PROTEIN (FRAGMENT).
601 YKSPFNHTTTVNTI-NSIH----SSVHEPLLIRMNSKDNVQETQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-2000) to the EMBL/GenBank/DDBJ dEMBL; AL137451; CAB70743.1; -
InterPro: IPR003598; Ig_-c2.
InterPro: IPR003598; Ig_-c2.
InterPro: IPR00306; Ig_-MHC.
InterPro: IPR001611; LRR.
InterPro: IPR003592; LRR_cterm.
InterPro: IPR003592; LRR_cterm.
InterPro: IPR003592; LRR_cterm.
InterPro: IPR003591; LRR_typ.
InterPro: IPR003591; LRR_typ.
InterPro: IPR003592; LRR_typ.
InterPro: IPR00404; IST.
InterPro: IPR00404; IST.
InterPro: IPR00404; IST.
INTS; PR000404; IST.
INTS; PR000404; IST.
INTS; PR000370; LRR; I.
SWART; SW00370; LRR; I.
SWART; SW00380; LRR_TYP; Z.
PROSITE; PS00227; TUBULIN; UNKNOWN_I.
NON TERFICAL PROTEIN; Immunoglobulin domain.
                                                                                                                                                                                           422
                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45110 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 62.6 tes 256; Conservative
                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               422 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-AMYGDALA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTPVVDW----
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480 YAQVQDNGTYLCIAANAGGNDSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTR 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDTMTPNCLYGLNLTSLSTTHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMLHELL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RDRKAQQVFVDEGHTVQFVCRADGDPPPAILWLSPRKHLVS-AKSNGRLTVFPDGTLEVR 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NVTVQDTGMYTCMVSNSVGNTTASATLNVTA-ATTTPFSYFSTVTVETMEPSQDEARTTD 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------LIKLDELDLSGNHLSAIRPGSFQGLM 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 HLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHNPW 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 NCNCDILWL---SWWIKDMAPSNTACCARCNTPPNLKGRYIGE----LDQNYFTCYAPVI 356
299 TIDKMQTSLDEVMKTTKIIIGCFVAVTLLAAAMLIVFYKLRKRHQQRSTVTAARTVEIIQ 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 RSMPSPLLACWQPILLLVLGSVLSGSATGCPPRCECSAQDRAVLCHRKRFVAVPEGIPTE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 RALFDPLLVVLLALQLLVVAGLV - RAQTCPSVCSCSNQFSKVICVRKNLREVPDGISTN 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISHWPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357 VEPPA-DLNVTEGMAAELKCRA-STSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFT
                              571 VDDEITGDTPM-----ESHLPMPAIEHEHLNHYNSYKSPFNHTTTVNTI-NSIH
                                                                                                                                                                                                                                                                                                                Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-BRAIN, AND ANAPLASTIC OLIGODENDROGLIOMA WITH 1P/19Q LOSS;
Strausberg'R.;
Submitted (JUL. 2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011057; AAH11057.1; -.
SEQUENCE 614 AA; 69145 MW; EFD967E3B716698D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 17.4%; Score 583.5; DB 4; Length 614; Best Local Similarity 27.7%; Pred. No. 6.8e-35; Matches 182; Conservative 96; Mismatches 241; Indels 137;
                                                                                                                                                                                                                                                                                                           Eukaryori, Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                 096FE5 PRELIMINARY; PRT; 614 AA. 096FE5; 01-DEC-2001 (TrEWBLrel. 19, Created) 01-DEC-2001 (TrEWBLrel. 19, Last sequence update) 01-DEC-2001 (TrEWBLrel. 19, Last annotation update) UNKNOWN (PROTEIN FOR MGC:17422).
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                                                                                           ---SSVHEPLLIRMNSKDNVQETQI 640
                                                                                                        417 PTVTTISEPYIIQTHTKDKVQETQI 441
                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAHNNLTLLPHDLFTPLHHLERIHLHNPWNCNCDILWLSWWIKDMAPSNTACCARCNTP 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAELKCRASTSLTSVSWITPNGTV 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGNTTASATLNVTAA--TTTPF 451
 301 PITIDGVWGGGRPGDAAGPASSSITAPAPRSSRPIEKAFIVPIIDVIENALKDLDDVMKIT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22; Gaps
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LSHASRHPRISVLNDGTLNFSRVLLIDTGVYTCMVTNVAGNSNASAYLNVSSAELNTPNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQSTRSTEKTFTIPVTD
                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 441;
                              Indels
                                                                                                                                                                                                                                                                                                                             Wang J., Bin L., Li G.;
"Brain tumor-associated mRNA.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF290542; AAG60620.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E2D17AB4607AC475 CRC64;
                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 1153; DB 11;
; Pred. No. 3.3e-77;
83; Mismatches 116;
                                                                                                                                          441 AA.
                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000483; LRR_Cterm.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48844 MW;
                                                                                                                                                                                                                   LIBG-LIKE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003599; Ig.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00409; IG; 1.
SMART; SM00408; IGC2; 1.
SMART; SM00410; IG_like; 1.
SMART; SM00370; LRR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 34.3%,
Best Local Similarity 50.3%
Matches 224; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001611; LKR.
InterPro; IPR000483; LKR_C
InterPro; IPR003592; LKR_O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SM00082; LRRCT; 1.
SM00369; LRR_TYP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; 19; 1.
Pfam; PF00560; LRR; 2.
Pfam; PF01463; LRRCT; 1.
                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin domain.
                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          441 AA;
                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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SMART; SM00
SMART; SM00
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SEQUENCE
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LRR_Cterm
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Ig_like.
Ig_MHC.
LRR.
                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003599;
InterPro; IPR003598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000483;
IPR000372;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR001611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P23945; 1XUN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               NCB1_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dayashizaki Y.;
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             562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRILNIHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 TIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RSMPSPLLACWQPILLLVLGSVLSGSATGCPPRCECSAQDRAVLCHRKRFVAVPEGIPTE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 RALFDPLLVVLLALQLLVVAGLV--RAQTCPSVCSCSNQFSKVICVRKNLREVPDGISTN 77
                                                                                                                                                                                                                                                                         Terao
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 69.2 KDA PROTEIN.
MAGAGA fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota: Metacos: Chordata; Craniata: Vertebrata; Eutheria: Primates; Catarrhini; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISHWPY
                                            563 LGVVLFCLVLLFLWSRGKGNTKHNIEIEYVPRKSDAGIS----SADAPRKFNMKM 613
                               534 VAITLMAAVMLVIFY--KMRKQHHRQNHHAPTRTVEIINVDDEITGDTPMESHLPM 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 137;
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-CEREBELLUM CORTEX;
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M.,
                                                                                                                                                                                                                                                                                  Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AB046639; BAB03557.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. protein; Immunoglobulin domain.
614 AA; 69187 MW; BA6C8BC7C993BE9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.2%; Score 578.5; DB 6; 27.6%; Pred. No. 1.6e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NLRYLNLAMCNLREIP---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.6e-34;
                                                                                                             614
                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :96
                                                                                                                                                                                                                                                                                                                                                                                                IPR000372; LRR_Nterm.
IPR003592; LRR_out.
IPR003591; LRR_typ.
540 ATV-PFP-FDIKTLIIATTMGFIS--
                                                                                                                                                                                                                                                                                                                                                                                     LRR_Cterm.
                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003598; 19_c2.
InterPro; IPR003006; 19_MHC.
InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 27.6% Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SM00082; LRRCT; 1.
SM00013; LRRNT; 1.
SM00369; LRR_TYP;
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LRR; 9.
LRRCT; 1.
LRRNT; 1.
                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                             EMBL; ABO46639; BAE
HSSP; P23945; 1XUN.
                                                                                                                                                                                                                          NCBI_TaxID=9541;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047;
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                                                                                                                        09N008;
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                                                                                                             800N60
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Arakawa T., Hara A., Fukunishi Y., Koshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alizawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J., Sakuli F., Suzuki R., Tomita M., Wagner I., Washio T., Sakani K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Rostincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Saroki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wannishaw-Bonis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  480 YAQVQDNGTYLCIAANAGGNDSMPAHLHVRSYSPDWPHQPNKTFAFIPNQPGEGEANSTR 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        562
LDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMLHELL 305
                                                                                     244 HLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHNPW
                                                                                                                                                                                                                                                                                                                                   421 RDRKAQQVFVDEGHTVQFVCRADGDPPPAILWLSPRKHLVS-AKSNGRLTVFPDGTLEVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415 NVTVQDTGMYTCMVSNSVGNTTASATLNVTA-ATTTPFSYFSTVTVETMEPSQDEARTTD
                                                                                                                                                   306 RLQEIQLVGGQLAMVEPYAFRGLNYLRVLNVSGNOLTTLEESVFHSVGNLETLILDSNPL
                                                                                                                                                                                                                                                                     304 NCNCDILWL---SWWIKDMAPSNTACCARCNTPPNLKGRYIGE----LDQNYFTCYAPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                     357 VEPPA-DLNVTEGMAAELKCRA-STSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         474 NNVGPTPVVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCF
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         534 VAITLMAAVMLVIFY -- KMRKQHHRQNHHAPTRTVEIINVDDEITGDTPMESHLPM 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  563 IGVVLFCLVLLFLWSRGKGNTKHNIEIEYVPRKSDAGIS----SADAPRKFNMKM 613
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EMBL; AK027262; BAB32403.1; -.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
ADULT MALE TESTIS CDNA. RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLONE:4930471K13, FULL INSERT SEQUENCE.
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MEDLINE=21085660; PubMed=11217851;
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SEQUENCE FROM N.A.
                                                                                                                         SEQUENCE FROM N.A.
                                                        NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                            SLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISHWPY 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCNCDILWL---SWWIKDMAPSNTACCARCNTPPNLKGRYIGE----LDQNYFTCYAPVI 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNVGPTPVVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCF 533
                                                                                                                                                                                                                                                                                                                                                                                                   -----LIKLDELDLSGNHLSAIRPGSFQGLM 243
                                                                                                                                                                                                                                                                                                                                                                                                                         246 LDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPIGTIEGSMLHELL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                              244 HLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHNPW 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEPPA-DLNVTEGMAAELKCRA-STSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFT 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
8438B23.1 (NEGRONAL LEUCINE-RICH REPEAT PROPEIN) (CDNA FLJ31810 FIS, CLONE NT2R12009289, WEAKLY SIMILAR TO CARBOXYPEPTIDASE N 83 KDA
                                                                                                                                                                                                                                                               TRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLT 137
                                                                                                                                                                                                                                                                                                           TIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLS 197
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                 20 RALFDPLLVVLLALQLLVVAGLV - - RAQTCPSVCSCSNQFSKVICVRKNLREVPDGISTN 77
                                                                                                                                                                                                                                                                                                                                                        NLRYLNLAMCNLREIP------
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                                                                                                                                                                                             95; Mismatches 243; Indels 137;
                                                                                                                                                                       DB 11; Length 614;
                                                                                                                                     AA; 69100 MW; 41CFF40C21335681 CRC64;
                                                                                                                                                                                Pred. No. 1.9e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            606 AA
                                                                                                                                                                       17.2%; Score 577.5; 27.6%; Pred. No. 1.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       540 ATV-PFP-FDIKTLIIATTMGFIS------
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                               Pfam; PF01463; LRRCT; 1.
Pfam; PF01462; LRRNT; 1.
SMART; SM00409; IG; 1.
SMART; SM00409; IGC2; 1.
SMART; SM00410; IG_11ke; 1.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRCT; 1.
                                                                                                     Immunoglobulin domain.
SEQUENCE 614 AA:
                                                                                                                                                                                 Best_Local Similarity 27.6%
Matches 181; Conservative
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         Pfam; PF00047;
Pfam; PF00560; 1
                                                                                                                                                                       Query Match
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A Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y., An Ishibashi T., Kanehori K., Tosida M., Yamashi T., Kanehori K., Tanai H., Tshida M., Yamashi H., Chiba Y., An Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J., An Hotuta T., Hiraoka S., Muraka H., Tshida H., Tshida H., Tshida H., Tshida H., Tshida H., Tshida T., Ishida M., Yamashita H., Cishida Y., Sugiyama T., Ishida K., Nakantra Y., Saito K., Nishikawa T., Amamoto J., Isono Y., Rawai-Hio Y., Saito K., Nishikawa T., An Magatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Magatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Submitted (Oct-2001) the EmBL/GenBank/DDBJ databases.

EMBL, AL353746; CAC2213.1; -

She EmBL, AR05372; BAB71167.1; -

InterPro; IPR003509; Ig_2.

InterPro; IPR003509; Ig_2.

InterPro; IPR001501; IRR_Cterm.

InterPro; IPR001501; IRR_Cterm.

InterPro; IPR001501; IRR_LYP.

InterPro; IRR017; IRRT; I.

InterPro; IRR017; IRRT; I.

InterPro; IRR017; IRRT; I.

InterPro; IRR017; IRRT; I.

InterPro; IRR01019; IRR_LYP.

IRR0175; IRR0175; IRRUF; I.

IRR0175; IRR0175; IRRUF; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 KELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAMCNLR 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 IKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFONRLTTIPNGAFVYLSKL 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 LALQLLVVAGLVRAQTCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQI 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAVVLIFMGSTI---GCPARCECSAQNKSVSCHRRRLIAIPEGIPIETKILDLSKNRLKS 71
                             Euteleostomi;
Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.1%; Score 575; DB 4; Length 606; 26.9%; Pred. No. 2.8e-34; Live 95; Mismatches 224; Indels 148;
                                                                                                                                                                                                                                                  to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CB608E281B066B9D CRC64;
                                 Craniata; Vertebrata; E
Catarrhini; Hominidae;
                             Chordata; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIUNTS: PRODOUGH LEURICHRPT.
SMART; SM00409; IG; 1.
SMART; SM00409; IG; 1.
SMART; SM00410; IG_like; 1.
SMART; SM0082; LRRCT; 1.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRUT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin domain.
SEQUENCE 606 AA; 68065 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 26.9%
Matches 172; Conservative
                                                                                                                                                                                                                Babbage A.;
Submitted (JAN-2001)
Homo sapiens (Human)
                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
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516

536

594

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RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Lip P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Lip P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Lip P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Lip P.W., Hoskins R.M., Henderson S.N.,
RA Burdon R.C., Rogers Y.H.C., Blazel R.G., Champe M., Heiglifer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Bullew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Buttls K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Dodgon K., Doug L.E., Downes M., Dugan-Rocha S., Dunn P.,
RA Borbon K., Borngelista C.C., Ferraz C., Ferriare S., Fleischmann W.,
RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Hostin D., Houston K.A., Howland T.J., Wel M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wel M.-H., Ibegwam C.,
Ra Jalli M., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai Z.,
Ra Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Rimmel B.E., Kodira C.D., Kraft C., McLeod M.P., McPherson D.,
R. Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
                                                                                                                                                                                                                                                 363 AGEATQIVDLHIIKLPHLLNSTNHIHEPDPGSSDISTSTKSGSNTSSSNGDTKLSQDKIV 422
                                                                                                                                                                                                                                                                                                                                         423 VAEATSSTALLKFNFQRNIPGIRMFQIQYNGTYDDTLVYRMIPPTSKTFL--VNNLAAGT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NERX OR BG:DS04862.1 OR CG4192.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Bukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
    ----RRLSREDDLETCASPPLLTGRYFWSIPEEEFLCEPPLITRHTHEMRVLEGQRAT
                                                                                                                                                                                                                                                                                                                                                                                -----TKIII--GCFVAI
                                                                                                                                                                                                                                                                                                                                                                                                                      481 MYDLCVLAIYDDGITSLTATRVVGCIQFTTEQDYVRCHFMQSQFLGGTMIIIIGGIIVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
                                                                                                                                          373 LKCRA-STSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNS
                                                                                                                                                                                 LRCKARGDPEPAIHWISPEGKLISNA---TRSLVYDNGTLDILITTVKDTGAFTCIASNP
                                                                                                                                                                                                                        432 VGNTTASA-----TLNVTAATTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                             537 TLMAAVMLVIFYKMRKQHHRQNHHAPTRTVEIINVDDEITGDTPMESHLPMP-----AI
                                                                                                                                                                                                                                                                                                    -TEKTFTIPVTDINSGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1021 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                  DWETTNVTTSLTPQSTRS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ephydroidea; Dro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BERKELEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           591 EHE 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                595 GHE 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09V430;
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KEK3
                                                                                                                                                                                                                                                                                                    483
                                                             313
                                                                                                     252
                                                                                                                                                                                 306
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                                                                                                                                          δ
                                                                                                                                                                               QQ
                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                           QQ
                                                                                                                                                                                                                                                                                                  δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ninomyya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H., Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishi S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsamura Y., Sekine M., Kikuchi H., Murakawa K., Kamehori K., Takahashi-Fuji A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

Submitted (OCT-2001).
311 TIEPHSFQGLRFLRVLNVSQNLLETLEENVFSSPRALEVLSINNNPLACDCRLLWILQRQ 370
                                       313 -SWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQN----YFTCYAPVIVEPPAD-LNVT 366
                                                                                                                   EGMAAELKCRASTSLTSV-SWITPNG---TVMTHGAYKVRIAVLSDGTLNFTNVTVQDTG 422
                                                                                                                                            MYTCMVSNSVGNTTASATLNVTAATTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVV 482
                                                                                                                                                                                                                                                                              DWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAV 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTIPNGAFVY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAM 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNL 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 PTLQFGGQQP-----MCAGPDTIRERSFKDFHSTALSFYFTCKKPKIREKKLQHLLVD 423
                                                                                                                                                                                                                                                                                                               DLKTILVSTAM-------GCFTFLGVVLFC 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---HLHHNPWNCNCDILWL 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 167; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 VLLALQLLVVAGLVRAQTCPSVCSCS--NQFSKVICVRKNLREVPDGISTNTRLLNLHEN 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ30803 FIS, CLONE FEBRA200125, WEAKLY SIMILAR TO NAG14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.3%; Score 480.5; DB 4; Length 719; 25.5%; Pred. No. 3.5e-27; Live 78; Mismatches 249; Indels 167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSNLHHLILNNNQLTLISSTAFDDV--------
                                                                                                                                                                                                                                                                                                                                                                              267 QSLVEINLAHNNLTLLPHDLFTPLHHLERI------
                                                                                                                                                                                                                                                                                                                                                        MLVIFYKMR-KQHHRQN---HHAPTRTVEIINVDDEITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 25.5%
Matches 169; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91N960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91N960
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
                                                                                                                                                                                                                                                                                                                 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122
                                                                                                                   367
                                                                                                                                                        424
                                                                                                                                                                                               423
                                                                                                                                                                                                                                      480
                                                                                                                                                                                                                                                                              483
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셤
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LANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGEL 182

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Db
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Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
A Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
A Relson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittana G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
A Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
Syleskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhon G.A.,
A Te J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zheng L.,
A Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

STRAINEY, AND CN BW SP,

Gelliker S.E., Agbayani A. Arcaina T.T., Baxter E., Blazej R.G.,

Butenhoff C., Champe M., Chavez C., Chew M., Clealolka L., Doyle C.M.,

Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,

Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,

Lewis S., Li.P., Lomorean M.A., Mazda P., Moshrefi A.R., Moshrefi M.,

Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,

Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,

Zieran L.L., Rubin G.M.;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AE003648; AAF5467.1;

EMBL, AE003413, AAF44948.1;
                                                                                                                                                                                                                                                                                                                                     STRAIN-Y, AND CN BW SP;
STRAIN-Y, AND CN BW SP;
STRAIN-99403001; Pubmed-10471707;
Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
Boyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
Palazzolo M., Rese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.
Celniker S., Rubin G.M.;
"An exploration of the sequence of a 2.9-Mb region of the genome of Drosophila melanogaster: the Adh region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.9%; Score 466; DB 5; Length 1021;
30.6%; Pred. No. 6.6e-26;
ive 57; Mismatches 157; Indels 108; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 GPRFNRALFDPL----LVVLLALQLLVVA---GLVRAQTCPSVCSCSNQFSK--VICVR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 GPRPQRRLHPPLRPRLPLHLHLLIMLLCCCSQLGQLRAE-CPAVCECKWKSGKESVLCLN 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00369; LRR_TYP; 2.
Immunoglobulin domain.
SEQUENCE 1021 AA; 109770 WW; 23CB5712EFD60969 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000483; LRR_Cterm.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003592; LRR_Out.
InterPro; IPR003591; LRR_Cut.
Pfam; PP00047; 19; 1.
Pfam; PF00047; 19; 1.
SWART; SW00408; LRR; 6.
SWART; SW00370; LRR; 2.
SWART; SW00310; LRR; 2.
SWART; SW00082; LRR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0028370; kek3.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR001611; LR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetics 153:179-219(1999).
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Best Local Similarity
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302
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                                                                                                                                                                     303 WNCNCDILWL-SWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nagase T., Ishikawa K., Kikuno R., Hirosawa M., Nomura N., Ohara O., "Prediction of the coding sequences of unidentified human genes. XV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 6:337-345(1999).
EMBL; AB033072; BAA86560.1; -.
243 MHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHNP
                                                                                                                                                                                       -----ASLHGLE---LARNT
                                                                                                                                                                                                                                    362 DLNVTEGMAAELKCRA-STSLTSVSWITPNGTVMTHGA-----YKVRIAVLSDG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KIAA1246.
Mimo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                            183 KRLSYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9B0E80F7BFF974A8 CRC64;
                                                                                                                                                                                                                                                                                                                 386 VVNMLRNASNLTILTADMQDAGIYTCAAENKAGKVEASVTLAVS 429
                                                                                                                                                                                                                                                                                                 ----TLNFTNVTV-----QDTGMYTCMVSNSVGNTTASATLNVT 444
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR001611; IRR.
InterPro; IPR000483; IRR_Cterm.
InterPro; IPR000372; IRR_NEWERT.
InterPro; IPR003592; IRR_NEWERT.
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Pfam; Pr005060; LRR; 7.
Pfam; Pr001469; LRRCT; 1.
PRINTS; PR00019; LECRICHRPT.
SMART; SM00408; IGC2; 1.
SMART; SM00408; IGC2; 1.
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Pfam; PF00047; ia: 1.
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NON_TER 1 1
SEQUENCE 832 AA; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=BRAIN;
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SMART; SM00370;
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SMART; SM00369;
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                          18;
                                                                                                             |::||| :| ODLETCGSPGGLKGRYFWHVREEEFVCEPPLITOHTHKLLVL 344
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                                                                                                                                              TIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLS 197
                                                                                                                                                                                                         IAEGTFADLOKLARLDLTSNRLOKLPPDPIFARSQASALTATPFAPPLSFSFGGNPLHCN 290
                                                                                                                                                                                                                                                                                          CDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVT 366
                                                                                                                                                                                                                                                                                                                                         EGMAAELKCRA-STSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     524 KTTKIII--GCFVAITLMAAVMLVIFYKMRKQHHRQNHHAPTR-TVEIINVDDEITGDTP 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLGEDTLRGLVNLQHLIVNNN-----------QLGGIADEAFEDF- 190
                                                                                                                                                                                                                                           IERNAFDNLQSLVEINLAHNNLTLLPHD-LF-----TPLHHLERIHLHNPWNCN 306
                                                                                                                                                                                                                                                                                                                                                                                                                  461
                                                                                                                                                                                                                                                                                                                                                                                                                                                               462 KSPPERAVLVSEVTTTSALVKWSVSKSAPRVKMYQLQYNCSDDEVLIYRMIPASNKAFVV 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNLVSGTGYDLCVLAMWDDT--ATTLTATNIVGCAQFFT-----KADYPQCQSMHSQIL 573
                                                                                              TRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLT 137
                                               RALFDPLLVVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKV--ICVRKNLREVPDGISTN 77
                                                                      37 OALSDOTMETLIGGLLAFGMAFAVVDACPKYCVCQNLSESLGTLCPSKGLLFVPPDIDRR 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECUENCE FROM N.A.
TISSUE-FRONTAL LOBE LEFT;
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao I
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA libraries.";
                                                                                                                                                                                                                                                                                                                                                         NLRYLNLAMCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQV
                                                                                                                                                                                                                                                                                                                                                                                          CMVSNSVGNTTASATL -----NVTAATTTPFSYFSTVT -------
                                                                                                                                                                                                                                                                                                                                                                                                                 CIAANAAGEATAMVEVSIVOLPHLSNSTSRTAPPKSRLSDITGSSKTSRGGGGSGGEPP
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 84.7 KDA PROTEIN
MACACA fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota: Metacos: Chordata; Craniata: Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
  Length 832;
                          Indels
13.2%; Score 442.5; DB 4;
24.5%; Pred. No. 2.7e-24;
Live 87; Mismatches 245;
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                         Conservative
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            Similarity
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                       164;
Query Match
Best Local
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                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRY 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPT----PVVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGI----DEVMKTTK 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                III--GCFVAITLMAAVMLVIFYKMRKQHHRQNHHAPTR-TVEIINVDDEITGDTPMESH 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERAVLVSEVTTTSALAKWSVSKSTPRVKMYQLQYNCSDDEVLIYRMIPASNKAFVVNNLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 RLGGNFIIHISRODFANMTGLVDLTLSRNTISHIQPFSFLDLESLRSLHLDSNRLPSLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LNLAMCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311 WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 789;
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(MAR-2001) to the EMBL/GenBank/DDBJ databases 6799; BAB39323.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                         1 protein; Immunoglobulin domain.
789 AA; 84730 MW; BB86DE81BC284B23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.0%; Score 437.5; DB 6; 24.5%; Pred. No. 6e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88; Mismatches
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                                                                                                                                    LRR_Cterm.
LRR_Nterm.
LRR_out.
                                                                                  19_c2.
19_MHC.
LRR.
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Pfam; PF01463; LRRCT; 1.
PRINTS; PR00019; LEURICHRPT
                                                                                                                                                                                                                                                                                            SM00060; FN3; I.

SM00409; IG; I.

SM00408; IGC2; I.

SM00370; LRR; 5.

SM0082; LRRCT; I.
                                                                                                                                                                                                                                                                                                                                                                SM00082; LRRCT; 1.
SM00013; LRRNT; 1.
SM00369; LRR_TYP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 24.5
                                                                                                                                                                      InterPro; IPR003592; LF
InterPro; IPR003591; LF
Pfam; PF00041; fn3; 1.
Pfam; PF00047; ig; 1.
                                                                                                                     InterPro; IPR001611; InterPro; IPR000483; InterPro; IPR000372; I
                                                   InterPro; IPR003961;
                                                                     IPR003599;
IPR003598;
                                                                                                      IPR003006;
                EMBL; AB056799; BAE
HSSP; P56276; lTLK.
                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical
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Matches 163;
                                                                     InterPro;
                                                                                    InterPro;
                                                                                                    InterPro;
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SMART;
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SMART;
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SMART;
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353 APVIVEP--PADLNVTEGMAAELKCRASTS-LTSVSWITPNGTVMTHGAYKVRIAVLSDG 409
                                                                                                                                                                                                                                                                                                                                                                            410 TLNFTNVTVQDTGMYTCMVSNSVGNTTASATLNVTAATTTPFSYFSTVTVETMEPSQDEA 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        530 IGCFVAITLMAAVMLVIFYKMRKQHHRQNHHAPTRTVEIINVDDEITGDTPMESHLPMPA 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----QIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERI 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bloecker H., Boecher M., Brandt P., Mewes H.W., Well B., Wlemann S.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                 RTIDNNVGPIPVVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               514 FPQDNN----NSVLVSWKA-
                                                                                     301 AVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTIESLPNLKEI
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                 HLHHNPWNCNCDILWLSW----WIKDMAPSNTACCARCNTPPNLKGRYIGELD-QNYFTCY
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T "Human neuronal leucine-rich repeat protein-3(NLRR-3).";

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AL442092. CAC09450.1;

R EMBL; AB060967; BA847184.1;

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig.

R InterPro; IPR003699; I.R.

R InterPro; IPR003691; LRR.

R InterPro; IPR003791; LRR.

R InterPro; IPR003591; LRR.

R INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-WAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 79.4 KDA PROTEIN (NEURONAL LEUCINE-RICH REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      708 AA.
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IYQKNRKKCVNVTTKGLHPDQKEYEKNNTTTL 626
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PÉRM; PF00047; ig; 1.
PÉRM; PF00606, LRR; 9.
PÉRM; PF01463; LRRCT; 1.
PÉRM; PF01462; LRRCT; 1.
PERM; PR010619; LEURICHRPT.
SMART; SM00060; FIS; 1.
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DKFZP761K2424 OR NLRR-3.
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Q9H3W5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGISTNTRLLNLHENQIQIIK-----VN----VN----SFKHLRHLEILQLS, 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----LTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKLWM-----1QS- 253
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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ilarity 24.0%; Pred. No. 1.3e-23;
Conservative 104; Mismatches 250; Indels 172;
Murray J., Langston Y., Clarke C.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; ACCO4142, AACCO752.1;
InterPro; IPR003961; FN_III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA; 79049 MW; 9B46066693F4BC1A CRC64;
                                                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RG118DO7.1.
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| IPR003006; Ig_MHC.
| IPR001611; LRR.
| IPR0000483; LRR_Cterm.
| IPR000372; LRR_Nterm.
| IPR003592; LRR_Out.
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SMART; SM00408; IGC2; 1.
SMART; SM00370; LRR; 4.
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Pfam; PPC00047; ig; 1.
Pfam; PPC00560; LRR; 9.
Pfam; PPC01463; LRRCT; 1.
Pfam; PPC01462; LRRUT; 1.
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SMART; SM00013; LRRNT; 1.
                                                                                                                                                                                                                                                                                         PRELIMINARY;
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SEQUENCE 705 AA; 79
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SEQUENCE FROM N.A.
TISSUE=FIBROBLAST;
                                                                                   585 LPMPA 589
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Best Local Simi
Matches 166;
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65 ARLPANTQILLLQTNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE 124
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                                                                                                                                                                                                                                                                                                                                                                                                            304 AVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTIESLPNLKEI 363
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                                                                                                                                                               Query Match 12.8%; Score 432; DB 4; Length 708;
Best Local Similarity 24.0%; Pred. No. 1.3e-23;
Matches 166; Conservative 104; Mismatches 250; Indels 172; Gaps
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           SWART; SM00370; LRR; 4.
SWART; SM00082; LRRCT; 1.
SWART; SM00013; LRRNT; 1.
SWART; SM00369; LRR_TYP; 1.
Hypothetical protein; Immunoglobulin domain.
SEQUENCE 708 AA; 79424 MW; 24710478D6B124D1 CRC64;
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598 IYQKNRKKCVNVTTKGLHPDQKEYEKNNTTTL 629
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                                                                                                                                   25 PLLV-VLLALQL-LVVAGLVRAQTCPSVCSCS------NQFSKVICVRKNLREVP 71
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APPLICANT: Corley, Neil C.
APPLICANT: Gorley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Batterson, Chandra
TITLE OF INVENTION: EXTRACELLULAR ADHESIVE PROTEINS
FILE REFERENCE: PF-0576 US
CURRENT FALLING DATE: 1998-08-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PERL Program
SEQ ID NO 2
LENGTH: 708
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           US-08-442-063A-27

US-08-272-919-2

US-08-619-916-2

PCT-US95-08542-2

US-08-458-834-4

US-08-458-834-4

US-08-458-834-4

US-08-119-2628-6

US-08-119-2628-6

US-08-119-2628-6

US-08-119-2628-6

US-08-119-2628-6

US-08-119-3628-1

US-08-334-265A-11

US-08-985-335-3

US-08-985-335-3

US-08-458-834-3
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09131648
Partent No. 6168920
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: 2687731
US-09-131-648-2
TYPE: PRT
ORGANISM: Homo sapiens
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 RESULT 1
US-09-131-648-2
 Query Match
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1 MINKWILHPQQIMIGPRFNR......VHEPLLIRMNSKDNVQETQI
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
                              Compugen Ltd
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US-08-986-485-5

US-08-196-485-2

US-09-191-647-2

US-09-191-647-2

US-09-18-30-305

US-09-18-30-305

US-09-18-930-305

US-09-18-930-305

US-09-18-930-305

US-09-18-950-2

US-09-18-950-2

US-09-182-024A-5

US-09-182-024A-5

US-09-182-024A-5

US-09-182-024A-5

US-09-083-950-4

US-08-195-006-2

US-08-190-802A-49

US-08-190-802A-49

US-08-477-346-50

US-08-477-346-50

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              GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                     August 26, 2002, 15:37:37
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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                                                                                                                               410 TLNFTNVTVQDTGMYTCMVSNSVGNTTASATLNVTAATTTPFSYFSTVTVETMEPSQDEA 469
                                                                                                                                                                                                                                                      304 AVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTIESLPNLKEI 363
                                                                                                                                                                                                                                  170 RTTDNNVGPTPVVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKII 529
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                                                                                                                                                                                                                                                                                                                            ----SSKILKSSVKWTAFVKTENSHAAQSARIPS-DVKVYNL-THLNPSTEYKICIDIPT 597
                                                                                                                                                                                        HLHHNPWNCNCDILWLSW---WIKDMAPSNTACCARCNTPPNLKGRYIGELD-QNYFTCY
                                                                                                          353 APVIVEP -- PADLNVTEGMAAELKCRASTS - LTSVSWITPNGTVMTHGAYKVRIAVLSDG
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APPLICANT: WU, SHUJIAN
APPLICANT: SWEET, RAYMOND
APPLICANT: TRUNEH, ALEMSEGED
TITLE OF INVENTYON: A HUMAN LIG-1 HOMOLOG (HLIG-1)
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAYMER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSCO for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: U8-DEC-1997
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598 IYQKNRKKCVNVTTKGLHPDQKEYEKNNTTTL 629
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APPLICATION NUMBER: 60/059,448
FILLING DATE: 22-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70264
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0701
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: linear
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COUNTRY: U
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                                                                                          LNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIP 140
                                                                                                                                                                                                                                                                         -----SYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDELDLSGNHLSAIRPG 237
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AFTGLDNLSKLTLFGNKIKSVAKRAFSGLESLEHLNLGENAIRSVQFDAFAKMKNLKELY
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                                               Indels 223;
    Length 1091;
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Patent No. 6046030
GENERAL INFORMATION:
APPLICANT: WU, SHUJIAN
APPLICANT: WWAYNOND
APPLICANT: TROWEH, ALEMSEGED
TITLE OF INVENTION: A HUMAN LIG-1 HOMOLOG (HLIG-1)
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
; Score 417.5; DB 3;
; Pred. No. 5.3e-27;
87; Mismatches 208;
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STREET: P.O. BOX 980
CITY: VALLEY FORGE
  12.4%; 23.1%;
                                               Conservative
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COMPUTER READABLE FORM:
                          Similarity
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STATE: PA
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                                               156;
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  Query Match
Best Local S:
Matches 156
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564 RIVEIINVDDEI-----TGDTP----MESHLPMPAIEHEHLNHYNSYKSPFNHTTTVN 612
                                                                                                                                                                                711 ----VVSVGETVALQCKATGNPPPRITWFKGDRPLSLTERHHL------TPDNQLLVVQ 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87 QIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVY 146
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451 FSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQSTRSTEKTFTIP-- 508
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                                    HD----ITIRTTTVARLECAATGH---PNPQIAWQKDGGTDFPAARERR----MHVMPDD
                                                                            ----VIDINSGIPGIDE-VMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQNHHAPT
                                                                                                    663 DVFFITDVKIDDAGVYSCTAQNSAGSISANATLTVLETPSLVVPLEDR------
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                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: GOodman, Corey
APPLICANT: Rid, Thomas
APPLICANT: Rid, Thomas
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/191,647
CURRENT APPLICATION NUMBER: 60/065,544
EARLIER PELLING DATE: 1997-11-14
EARLIER PELLING DATE: 1997-11-14
EARLIER FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 14
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; Patent No. 6046015
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; ORGANISM: human
US-09-191-647-2
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.9%; Score 401; DB 3; Length 1101; Sest Local Similarity 22.0%; Pred. No. 1.4e-25; Matches 172; Conservative 111; Mismatches 265; Indels 234; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 LLVVLLALQLLVVAGLVRAQTCPSVCSCSNQ----FSKVICVRKNLREVPDGISTNTRL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 LWLLLLRLEPVTAAAGPRA-PCAAACTCAGDPCTCAGDSLDCGGRGLAALPGDLPSWTRS 79
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                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                      PAPLICATION NUMBER: US/08/986,485
FILING DATE: 08-DEC-1997
CLASSIPECATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 60/059,448
FILING DATE: 22-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70264
TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                  TELBERN: 846169
INFORMATION FOR SEQ 1D NO: 2: SEQUENCE CHARACTERISTICS:
**RNGTH: 1101 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-986-485-2
                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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365 TELPKSLFEGLFSLOLLLLNANKINCLRVDAFQDLHNLNLLSLYDNKLQTIAKGTFSPLR 424
                                          292 HLERIHLHHNPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTC 351
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                                                                                                                                                                                                                                                                                                       Faceur No. 0.4.0994

GENERAL INFORMATION:
APPLICANT: Goodman, Corey
APPLICANT: Tododman, Corey
APPLICANT: Todofman, Corey
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,245A

CURRENT FILING DATE: 2000-03-31
PRIOR FILING DATE: 1997-11-14
PRIOR FILING DATE: 1997-11-14
PRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver: 2.0
                                                                                                                            352 YAPVIVEPPADLNVTEGMAAELKCRASTSLTSVS 385
                                                                                                                                                                    483 SGTEDYRSKLSGDCFADLACPEKCRCEGTTVDCS 516
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; ORGANISM: human
US-09-540-245A-2
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87 QIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVY 146
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                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Goodman, Corey
APPLICANT: Goodman, Corey
APPLICANT: Goodman, Corey
APPLICANT: Brose, Katja
APPLICANT: TESSier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT FILING DATE: 2000-03-31
PRIOR FILING DATE: 1998-011-13
PRIOR FILING DATE: 1998-11-13
PRIOR FILING DATE: 1998-104-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2: Learner
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25.1%; Pred. No. 6.7e-25;
ive 51; Mismatches 171;
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352 YAPVIVEPPADLNVTEGMAAELKCRASTSLTSVS 385
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                                          483 SGTEDYRSKLSGDCFADLACPEKCRCEGTTVDCS
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Best Local Similarity 25.1%
Matches 129; Conservative
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; ORGANISM: human
US-09-540-153-2
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                                         GENERAL INFORMATION:

APPLICANT: Connolly, Timothy
APPLICANT: Connolly, Timothy
APPLICANT: Manu
TITLE OF INVENTION: Bhanu
TITLE OF INVENTION: Same
CURRENT APPLICATION NUMBER: U5/09/182,024A
CURRENT APPLICATION NUMBER: 06/063,946
PRIOR APPLICATION NUMBER: 60/063,946
PRIOR APPLICATION NUMBER: 60/064,420
PRIOR APPLICATION NUMBER: 60/096,420
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 1523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 RILVTSFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLRQRRTVGQFTLCMAPVHLRGFNVA 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | || :| :| | | :| 318
315 EQNSIKAIPAGAFTQYKKLKRIDISKNQISDIAPDAFQGLKSLTSLVLYGNKITEIAKGL 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --GLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299 HHNPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVE 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 LALQLLVVAGLVRAQTCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQI 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 176;
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1523;
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 11.3%; Score 381; DB 4; Lo
Best Local Similarity 25.0%; Pred. No. 1.2e-23;
Matches 138; Conservative 56; Mismatches 183;
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            Sequence 2, Application US/09182024A Patent No. 6342370
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541 DNEVSVLEATGIF 553
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US-09-182-024A-2
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Sequence 305, Application US/09188930A Patent No. 6150502

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Best Local Similarity 23.4%; Pred. No. 4.7e-24;
Matches 165; Conservative 109; Mismatches 252; Indels 178;
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
TITLE OF INVERTION: Compositions Isolated From Skin Cells
TITLE OF INVERTION: COMPOSITIONS FOR Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
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LENGTH: 649
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LENGTH: 1480
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                                                                  GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: MEI-019
CURRENT APPLICATION NUMBER: US/09/063,950C
CURRENT FILING DATE: 1998-04-21
NUMBER OF SEO ID NOS: 9
SOFTWARE: PAtentin Ver. 2.0
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APPLICANT: Goodman, Corey
APPLICANT: Goodman, Corey
APPLICANT: Brose, Katja
APPLICANT: Brose, Katja
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/191,647
CURRENT FILING DATE: 1998-11-13
EARLIER APPLICATION NUMBER: 60/065,544
EARLIER FILING DATE: 1997-11-14
EARLIER FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver: 2.0
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Patent No. 6046015
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                                                                                                                                                                                                                                 SEQ ID NO 2
LENGTH: 673
                 US-09-063-950-2
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46 TCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEIL 105
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                                                                                                                                                                                                                                                                                                                  294 SCPHPCRCADGI -- VDCREKSLTSVPVTLPDDTTDVRLEQNFITELPPKSFSSFRRLRRI 351
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                                                                                                                                             Query Match 10.4%; Score 350; DB 3; Length 1480; Best Local Similarity 23.9%; Pred. No. 5.1e-21; Matches 109; Conservative 65; Mismatches 152; Indels 130;
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APPLICANT: Bross, Katja
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REPERENCE: B98-031-3
CURRENT PILIOR DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/065,544
PRIOR APPLICATION NUMBER: 60/065,544
PRIOR FILING DATE: 1997-11-14
PRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 20
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TYPE: PRT; ORGANISM: Drosophila melanogaster
US-09-191-647-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT CRGANISM: Drosophila melanogaster US-09-540-245A-7
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APPLICANT: Goodman, Corey
APPLICANT: Kid, Thomas
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Sequence 2, Application PC/TUS9109055
GENERAL INFORMATION:
APPLICANT: Rothberg, Jonathan Marc and Artavanis-Tsakonas, Spyridon
TITLE OF INVENTION: Purified SLIT protein and Sequence Elements Thereof
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                       412 DAFRDLHSLSLISLYD-NNIQSLANGTFDAMKSMKTVHLAKNPFICDCNLRWLADYLHKN 470
                                                                                                                                                                  531 DCTGRRLKEIPRDIPLHTTELLINDNELGRISSDGLFGRLPHLVKLELKRNQLTGIEPNA 590
                                                                                                                                                                                                             239 FOGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHL 298
                                                                                                                                                                                                                                                                                            299 HHNPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVE 358
                                                                                   471 PIETSGARCESPKRMHRRRIESLREEKFKCSWGELRMKLSGECRMDSDCPAMCHCEGTTV
                                                                                                                                                                                                                                                                                                                      similarity to other signal
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                                                                                                                              ---IKLD-----
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ADDRESSEE: Office of Cooperative Research
STREET: 246 Church Street
STREET: Suite 401
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/624,135
FILING DATE: 7-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barth, Richard J.
REGISTRATION NUMBER: 28,180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTIFICATION METHOD: similarity to or OTHER INFORMATION: Directs Export NAME/KEY: Four Flank-LRR-Flank domains LOCATION: 37 to 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/09055
FILING DATE: 19911127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 972-1400
TELEFAX: (212) 370-1622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: signal sequence
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TELEX: 236268
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STATE: CC
COUNTRY:
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                         QLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPS 165
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APPLICANT: Goodman, Corey
APPLICANT: Goodman, Corey
APPLICANT: Tessler-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REPRENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,153
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/191,647
PRIOR APPLICATION NUMBER: 09/191,647
PRIOR APPLICATION NUMBER: 09/191,057
PRIOR PILING DATE: 1998-04-07
NUMBER OF SEO ID NOS: 14
SOFTWARE: PatentIn Ver: 2.0
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Patent.No. 6270995
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT : ORGANISM: Drosophila melanogaster US-09-540-153-7
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125; Conserva
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Best Local Similarity
Matches 109; Conserv
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Best Local S:
Matches 125
SOFTWARE:
SEQ ID NO 5
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APPLICANT: Rajput, Bhanu
TITLE OF INVENTION: Human Slit Polypeptide and Polynucleotides Encoding
TITLE OF INVENTION: Same
FILE REFERENCE: 640100-271
CURRENT APPLICATION NUMBER: US/09/182,024A
CURRENT APPLICATION NUMBER: 60/063,946
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 5
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Best Local Similarity 23.9%; Pred. No. 5.1e-21;
Matches 109; Conservative 65; Mismatches 152; Indels 130; Gaps
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                                             LOCATION. 911 to 1150

IDBNTIFICATION METHOD: similarity to tandem EGF-like
OTHER INFORMATION: protein-protein interactions
NAME/KEY: 7th EGF-like repeat
LOCATION: 1353 to 1393
IDBNTIFICATION METHOD: similarity to epidermal growth
OTHER INFORMATION: Involvement in receptor-ligand
NAME/KEY: Alternative splice segment
LOCATION: 1394 to 1404
IDBNTIFICATION METHOD: experimental
OTHER INFORMATION: developmentally regulated
                                                                                                                                                                                                                                                                                                                                               CTHER INFORMATION METHOD: experimental OTHER INFORMATION: developmentally regulated NAME/KEY: COOH-terminal region 1405 to 1480 in IDENTIFICATION METHOD: experimental PCT-US91-09055-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : | | : | : | | : | | : | | : | | | : | | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                  Tandem EGF-like repeats
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-182-024A-5
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Patent No. 6225085
GENERAL INFORMATION:
APPLICANT: HOLIZAMAN DOUGLAS A.
TITLE OF INVENTION: THEREFOR
FILLE REFERENCE: MEL-019
CURRENT APPLICATION UNBER: US/09/063,950C
CURRENT FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN Ver: 2.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                         352 DLSNNNISRIAHDALSGLKQLTTLVLYGNKIKDLPSGVFKGLGSLRLLLLNANEISCIRK 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 QLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPS 165
                                                                                                                                                                                                                                                46 TCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEIL 105
                                                                                                                                                                                                                                                                                                   294 SCPHPCRCADGI -- VDCREKSLTSVPVTLPDDTTDVLLEQNFITELPPKSFSSFRRLRRI 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:| |:|:| : :::|: | | | | | | | | ::|
591 FEGASHIQELQLGENKIKEISNKMFLGLHQLKTLNLYDNQISCVMPGSFEHLNSLTSLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HHNPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   471 PIETSGARCESPKRMHRRRIESLREEKFKCSWGELRMKLSGECRMDSDCPAMCHCEGTTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166 YAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAM-----CNLR-----
                                                                                                                                      10.3%; Score 347; DB 4; Length 1480;
ilarity 23.9%; Pred. No. 9.2e-21;
Conservative 65; Mismatches 152; Indels 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 286;
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TYPE: PRT
ORGANISM: Drosophila melanogaster
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λλ			. 08	
ą	67 RLPDGIPGGTQALWLDSNNLSSIPPAAFRNLSSLAFLNLQGGQLGSLEPQALLGLENLCH	GGOLGSLEPQALLGLENLCH	126	
λλ	81 INLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIP	NGLANLNTLELFDNRLTTIP	140	
q	127 LHLERNQLRSLAVGTFAYTPALALLGLSNNRLSRLEDGI	EGLGNLWDLNLGWNSLAVLP	186	
λγ	141 NGAFVYVYLSKLKELWLRNNPIESIPSYAFNRIPSLRR	NNPIESIPSYAFNRIPSLRR	176	
ą	187 DAAFRGLGGLRELVLAGNRLAYLQPALFSGLAELRELDLSRNALRAIKANVFAQLPRLQK	RNALRAIKANVFAQLPRLQK	246	
λλ	177 L		177	
ą	247 LYLDRNLIAAVAPGAFLGLKALRWLDLSHNRVAGLLEDTFPGLLGLRVLRLSHNAIASLR 306	PGLLGLRVLRLSHNAIASLR	306	
γ	178RLSYISEGAFEGISNLRY	RLSYISEGAFEGLSNLRY	201	
ą	307 PRIFEDLHFLEELQLGHNRIRQLAERSFEGLGQLEVLTLDHNOLQEVKVGAFLGLINVAV	HNOLOEVKVGAFLGLTNVAV	366.	
λλ	202 LNLAMCNLREIPNLTPLIKLDELDLSGNHLSAIRPGS	OGLMHLOKLWMIQSQIQVIE	. 622	
ą	367 MNLSGNCLRNLPEQVFRGLGKLHSLHLEGSCLGRIRPHTFAGLSGLRRLFLKDNGLVGIE	AGLSGLRRLFLKDNGLVGIE	426	
λλ	260 RNAFDNLQSLVEINLAHNNLTLLPHDLFTPL		290	
q	427 EQSLWGLAELLELDLTSNQLTHLPHQLFQGLGKLEYLLI	HNRLAELPADALGPLORAFW	486 1.	
λλ	291HH	-LERIHLHHNPWNCNCDILW	311	
qç	487 LDVSHNRLEALPGSLLASLGRLRYENLRNNSLRTFTPQF	GLERLWLEGNPWDCSCPLKA	546	
λ,	312 LSWWIKDMAPSNTACCAR	CNTPPNLKGRYIGELDONYF	349	
ð	547 LRDFALQNPSAVPRFVQAICEGDDCQPPVYTYNNITCASPPEVAGLDLRDLGEAHF	CASPPEVAGLDLRDLGEAHF	602	
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Search completed: August 26, 2002, 15:41:22 Job time: 225 sec

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(without alignments) ... 1681.764 Million cell updates/sec
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/SIDSI/gogdata/hold-geneseq/genesegp-embl/AA1981.DAT:
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/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:
                                                                                                                                                                                                                                                                August 26, 2002, 15:41:53; Search time 31.57 Seconds
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1 QTCPSVCSCSNQFSKVICVR......KTFTIPVTDINSGIPGIDEV
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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No.
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Homo sapiens WO9914241-A2 17-SEP-1998; 11-SEP-2000 25-MAR-1999 AAY08100; PR0331 prote prote polyp Human PRO331 prote protein (Clo acid sequenc PRO331 prote respo Human PR0331 Novel Human Human Human AAW85722 AAY13394 AAB24407 AAY70673 AAU12355 AAU00826 AAY08100

prote

Human Human

angiogenesis Human leucine-rich

Human

AAB65292 AAB53089 AAE13006

640 640 640 640 640 640 640

100.0 100.0 100.0 100.0 100.0 100.0 100.0

2524 2524 2524 2524 1793.5

0.00

prote

immune PR0331

cc359_4 secreted p	Human PRO1111 prot	Membrane-bound pro	Human sbgPRO331a p	Human PRO1111 poly	Human PRO1111 (UNQ	Human SLIT protein	Human 1mmunoglobul			Human cDNA SEQ ID	Human secreted pro	3 en	Human ORFX ORF2855	Human cDNA SEQ ID	Human immunoglobul	Human secreted pro		Amino acid sequenc	Mature human neuro	Human neuronal gui	membrane	Amino acid sequenc	Human PRO227 polyp	Human PRO227 prote	Human sbgTango79a	Amino acid sequenc			Amino acid sequenc	Human PRO293 prote	Polypeptide identi	Human ORFX ORF2277	Human protein SEQ
AAY28806	AAB24073	AAY66694	AAE09438	AAU12390	AAB65217	AAB23044	AAU18035	AAB23034	AAB23033	ABB10349	AAY87066	AAE06043	AAB43091	ABB10522	AAU18084	AAY87135	AAE06112	AAW84596	AAE06804	AAE06799	AAB74705	AAY13357	AAU12333	AAB80225	AAE09437	AAB31161	AAG67505	ABB60162	AAY13385	AAB80253	AAY02379	AAB42513	AAM78823
20	21	21	22	22	22	21	22	21	21	22	21	22	21	22	22	21	22	20	22	22	22	20	22	22	22	22	22	22	20	22	20	21	22
653	653	653	653	653	653	448	909	230	694	553	302	302	441	281	281	224	224	614	579	909	620	620	620	620	. 592	548	166	1021	713	713	707	705	705
62.7	62.7	62.7	62.7	62.7	62.7	61.9	61.8	61.4	61.4	53.7	38.5	38.5	35.1	33.5	33.5	27.1	27.1	22.5	22.4	22.4	22.4	22.0	22.0	22.0	20.7	18.9	17.9	17.6	17.1	17.1	16.7	16.7	16.7
1581.5	1581.5	1581.5	1581.5	1581.5	1581.5	1561.5	1560.5	1548.5	1548.5	1356.5	971	971	886.5	845.5	845.5	685	: 685	568.5	565.5	565.5	565.5	556.5	556.5	556.5	522.5	477.5	453	443.5	430.5	430.5	422.5	421	421
12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27.	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT

anti-inflammatory; anti-autoimmune; anti-diabetic; spondyloarthropathy; T cell-mediated disease; spondyloarthropathy; sclerosis; renal disease; inflammatory myopathy; hemolytic anemia: thrombocytopenia; thyroiditis; diabetes mellitus; demyelinating polyneuropathy; Guillain-Barre syndrome; multiple sclerosis; polyneuropathy; hepatitis; cirrhosis; enteropathy; sclerosing cholangitis; inflammatory bowel disease; Whipple's disease; skin disease; dermatitis; psoriasis; asthma; allergic rhinitis; tumor; food hypersensitivity; urticania; eosinophilic pneumonia; transplant; idiopathic pulmonary fibrosis; graft rejection; PRO245; human; Inflammatory cell infiltration; immune response; T cell proliferation; AAY08100 standard; Protein; 640 AA 97US-0059119. 97US-0059263. 97US-0063550. 97US-0065186. 98WO-US19437 (first entry) Human PRO331 protein. 17-SEP-1997; 18-SEP-1997; 28-OCT-1997; 12-NOV-1997; AAY08100

225 dlsgnhlsairpgsfqglmhlqklwmiqsqiqviernafdnlqslveinlahnnltllph 284

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This invention describes a novel composition containing (apart from a carrier or excipient), a novel PRO245 polypeptide (I), its agonist or antagonist, or their fragments, for modulating: (i) infiltration of antagonist, or their fragments, for modulating: (i) infiltration of inflammatory cells into tissue; (i) an immune response; or (iii) T cell proliferation. The composition increases or decreases any of the effects (I)-(ii). The products of the invention have anti-inflammatory, anti-autoimmune and anti-diabetic activity. (I), and its (ant)agonists and their fragments, are used to treat immune-related diseases, particularly T cell-mediated diseases. The diseases treated include systemic lupus erythematosus, rheumatoid arthritis, juvenile chronic arthritis, spondyloarthropathies, systemic solerosis (scleroderma), carthritis, spondyloarthropathies, systemic sclerosis (scleroderma), carthritis, spondyloarthropathies, systemic sclerosis (scleroderma), carthritis, autoimmune pancytopenia, paroxysmal nocturnal hemoglobinuria), autoimmune hemotytopenia, paroxysmal nocturnal hemoglobinuria), autoimmune hemotytopenia, paroxysmal nocturnal hemoglobinuria, juvenile lymphocytic thyroiditis, atrophic thyroiditis, diabetes mellitus, immune-mediated renal disease (dlomerulonephritis, juvenile lymphocytic thyroiditis, atrophic chypathic demyellnating polyneuropathy, Guillain-Barte syndrome, chronic active demyellnating polyneuropathy, infectious hepatitis crohn's disease, chronic active mepatitis, publiancy blilary cirrhosis, garanlommators chonic active mepatitis, inflammatory bowel disease contonic active hepatitis, inflammatory bowel disease solumnune mediated syndrespiect syndrespiect chronic active hepatitis, and sclerosing cholangitis, inflammatory bowel disease solumnune mediated syndrespiect contains and sclerosing erytheme or immune mediated solutis; sorchises and profilm mediated contains deniand disease sorchism and profilmine profilmine contains and sclerosing erytheme or immune contains deniant denian and account
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bullous skin diseases, erythema multiforme, contact dermatitis, psoriasis, sathma, allergic rhintis, atopic dermatitis, food hypersensitivity, urticaria, eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, and transplantation associated diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (graft rejection, and graft-versus-host-disease). (I), its (ant)agonists for fragment can also be used as an adjuvant in treatment of tumors. Antibodies against (I) can also be used for diagnosing such diseases. This sequence represents the human PRO331 protein which is described in
                                                                                                                                                                                                                                                                                                            Composition containing novel polypeptide PRO245, its agonist or
                                                                                                                                                                    Wood WI;
                                                                                                                                                                    Tumas D,
                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 33; 177pp; English.
                                                                                                                                                                    Gurney AL,
97US-0066364.
97US-0066770.
98US-0088026.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the method of the invention.
                                                                                                             (GETH ) GENENTECH INC.
                                                                                                                                                                 Goddard A,
                                                                                                                                                                                                                        WPI; 1999-229499/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  640 AA;
                                                                                                                                                                                                                                                     N-PSDB; AAX37738
  21-NOV-1997;
                                                      04-JUN-1998;
                                                                                                                                                                                                                                                                                                                                         antagonist
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                                                                                                            LQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIP 120
                                                                                                                                                          SYAFWIPSLRRLDUGELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDEL 180
                                                                     Gaps
                                                    1 QTCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEI 60
                           ;
0
100.0%; Score 2524; DB 20; Length 640; 100.0%; Pred. No. 2.4e-177;
                          0; Mismatches
                          Conservative
        Best Local Similarity
Matches 478; Conserv
Query Match
                                                                                                                                       105
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                                                                                                            61
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g S DLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLFLLPH 240

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The new human secreted proteins are encoded by polynucleotides obtained from human placenta, adult testes, fetal kidney, fetal adult brain, adult brain and adult blood cDNA libraries.

Expension adult brain and adult blood cDNA libraries.

The polynuclectides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as activity, tissue growth activity, activiti/inhibhla activity, chemotactic/chemokinetic activity, anti-inflammatory activity, activity, activity, and tumour inhibition activity, The polynucleotides are also stated to be useful for gene cativity. The sequences lidentified by a secretory leader contifining the polynucleotide and it is thought that the
                                                              VLSDGTLNFTNVTVQDTGMYTCMVSNSVGNTTASATLNVTAATTTPFSYFSTVTVETMEP 420
 241 DLFTPLHHLERIHLHHNPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGEL 300
                                                                                                                                                          405 visdgtinftnvtvqdtgmytcmvsnsvgnttasatinvtaatttpfsyfstvtvetmep 464
                                                                                                                                                                                                                      522
                                                                                                                                                                                         SQDEARTIDNNVGPTPVVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEV 478
                Polynucleotide; protein; nutrition; cytokine; cell proliferation; cell differentiation; immunostimulation; immunosuppression; demacatopoiesis regulation; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostaxis; thrombolysis; receptor; ligand; anti-inflammatory; tumour suppression; gene therapy.
                                                                                                                                           Lavallie ER;
Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides encoding secreted human proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C, Jacobs K,
Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 26; Page 109-111; 136pp; English.
                                                                                                                                                                                                                                                                                                  AAW85722 standard; Protein; 640 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J, Bowman MR, Evans C
Merberg D, Racie LA,
                                                                                                                                                                                                                                                                                                                                                                                               Novel protein (Clone AS209_1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-US22034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0955557.
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-288272/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAX08687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9920644-A1.
                                                                                                                                                                                                                                                                                                                                                                27-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-OCT-1997;
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McCoy JM, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-APR-1999.
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                                                                                                                                                                                DQNYFTCYAPVIVEPPADLNVTEGMAAELKCRASTSLTSVSWITPNGTVMTHGAYKVRIA 360
                                                                                                                                                                                                                                                                              361 VLSDGTLNFTNVTVQDTGMYTCMVSNSVGNTTASATLNVTAATTTPFSYFSTVTVETMEP. 420
                                                                                                                                                                                                                                                                                        encoded proteins have biological activity by virtue of their secreted nature. This polypeptide was encoded by a clone designated AS209_1 (See AAX08687).
                                                                                                                                                          DLFTPLHHLERIHLHNPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGEL 300
                                                                                                                                                                                                                                                         SYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDEL 180
                                                                                              Secreted protein; transmembrane protein; human; enterocolitis; zollinger-Ellison syndrome; gastrointestinal ulceration; congenital microvilus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alsheimer's disease; ALS; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair.
                                                                       Gaps
                                                                                     1 QTCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEI 60
                                                                                                                                                                                                                                                                                                              SQDEARTTDNNVGPTPVVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEV 478
                                                                                                                                                                                                                                                                                                                      ;
;
                                                      Query Match 100.0%; Score 2524; DB 20; Length 640; Best Local Similarity 100.0%; Pred. No. 2.4e-177; Matches 478; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of protein PR0331.
                                                                                                                                                                                                                                                                                                                                                                    AAY13394 standard; Protein; 640 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0066840.
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97US-0059115.
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                              640 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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17-SEP-1997;
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                                Sequence
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AAY13344-403 represent secreted and transmembrane human proteins. The cDNA sequences are obtained from cDNA libraries, prepared from fetal lung, fetal kidney, fetal liver and fetal retina. The encoded polypeptides have specific uses based on their homology to known polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the vulva and gllomas), potent effects on cell growth and development, diseases related to growth or survival of nerve cells including Parkinson's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ō
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yuan J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wood WI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated human genes and polypeptides used in,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pennica D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Fig 104; 320pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0063564.
97US-0063435.
97US-0063704.
                                                                                                                                                                                                                                                        97US-0063120.
97US-0063121.
97US-0063127.
                                                                                                                                                                                                                                                                                                                            97US-0063128.
97US-0063329.
97US-0063327.
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97US-0063544.
97US-0063549.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastrointestinal ulceration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0066364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen J, Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-229533/19.
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17. SEP - 1997

18. SEP - 1997

18. SEP - 1997

18. SEP - 1997

17. OCT - 1997

24. OCT - 1997

26. OCT - 1997

27. OCT - 1997

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28. OCT - 1997

29. OCT - 1997
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24-NOV-1997;
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07-NOV-1997
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Alzheimer's disease, ALS, neuropathles or cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can be used as an anti-thrombotic agent; PRO287 polypeptides and portions may have therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the Kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation; diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLFTPLHHLERIHLHNPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGEL: 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DONYFICYAPVIVEPPADLNVTEGMAAELKCRASTSLISVSWITPNGTVMTHGAYKVRIA 360,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLSDGTLNFTNVTVQDTGMYTCMVSNSVGNTTASATLNVTAATTTPFSYFSTVTVETMEP 420
                                                                                                                                                                                                                                                                                                                LQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIP 120
                                                                                                                                                                                                                                                                                                                                                           SYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDEL 180
                                                                                                                                                                                                                                                                                                                                                                           DLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPH 240
                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                          QTCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQDEARTTDNNVGPTPVVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEV 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 2524; DB 20; Length 640;
; Pred. No. 2.4e-177;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human PRO331 protein sequence SEQ ID NO:107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB24407 standard; Protein; 640
                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US28313
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                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 478; Conservative
                                                                                                                                     640 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200032221-A2.
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                                                                                                                                     Sequence
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The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, angiogenic disorder in mammals by modulating cell proliferation, and indiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with imappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atheroscierosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24388 to AAB2438 represent invention.
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Paoni NF, Smith V;
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                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals -
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Kuo SS,
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Klein RD, H
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Godowski PJ, Gurney AL, Kl
Watanabe CK, Williams PM,
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Best Local Similarity
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23-JUN-1999;
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                                         12-MAR-1999
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                                 VLSDGTLNFTNVTVQDTGMYTCMVSNSVGNTTASATLNVTAATTTPFSYFSTVTVETMEP 420
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te= "Casein Kinase II phosphorylation site"
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The present sequence is the human protein PRO331, encoded by UNO292 cDNA, designated as clone DNA40981. It is isolated from human foetal brain tissue. Portions of PRO331 has homology to the LIG-1 protein.

CI tenhances or suppresses the infiltration of inflammatory cells into tissues, proliferation of T-lymphocytes and modulates the immune response. This sequence is useful for treatment of immune related disorders, like SLE, rheumatoid/juvenile arthritis, spondyloarthropathy, systemic sclerosis (scleroderma), idiopathic inflammatory myopathies such systemic sclerosis (scleroderma), idiopathic inflammatory myopathies such cas dermatomyositis, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, thrombocytopenia, thyroiditis e.g. Grave's disease, diabetes mallitus, immune-mediated renal disease e.g. comerulonephritis, demyelinating diseases such as multiple sclerosis and cullar syndrome, hepatobiliary diseases like hepatitis and cullar plantar cirrhosis, inflammatory and fibrotic lung diseases such as inflammatory bowel disease (e.g. Crohn's disease), autoimmune or immunological diseases of the lungs such as sosinophilic pneumonia and transplantation associated diseases such as graft-versus-host-disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition for treatment and diagnosis of immune related diseases e.g. Grave's disease comprises a PRO245, PRO217, PRO301, PRO266, PRO335, PRO331 or PRO326 polypeptide or its agonists or antagonists (preferably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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re= "Casein Kinase II phosphorylation site"
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llarity 100.0%; Pred. No. 2.4e-177;
Conservative 0; Mismatches 0; Indels 0;
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"N-myristoylation site"
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                                                                                                                                                                                                                                                        Human secretory and transmembrane; PRO; mammallan; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.
                                                                    300
                                                                                              DQNYFTCYAPVIVEPPADLNVTEGMAAELKCRASTSLTSVSWITPNGTVMTHGAYKVRIA 360
                                                                                                     VLSDGTLNFTNVTVQDTGMYTCMVSNSVGNTTASATLNVTAATTTPFSYFSTVTVETMEP 420
                                                                                                                                 SQDEARTTDNNVGPTPVVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEV 478
                                                                                                                                                           105 lqlsrnhirtieigafnglanlntlelfdnrlttipngafvylsklkelwlrnnpiesip
                                                                    DLFTPLHHLERIHLHHNPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGEL
                                                                                                                                                                                                                                          Human PRO331 polypeptide sequence.
                                                                                                                                                                                                  AAU12355 standard; Protein; 640
                                                                                                                                                                                                                                                                                                                                                                                                                              2000WO-US03565.
2000WO-US04341.
2000WO-US04342.
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99WO-US30999
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2000WO-US05004
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2000WO-US13705
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18-FEB-2000;
18-FEB-2000;
22-FEB-2000;
24-FEB-2000;
24-FEB-2000;
01-MAR-2000;
                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                         02-DEC-1999;
09-DEC-1999;
16-DEC-1999;
20-DEC-1999;
30-DEC-1999;
06-JAN-2000;
06-JAN-2000;
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21-MAR-2000;
30-MAR-2000;
17-MAY-2000;
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01-DEC-1999;
02-DEC-1999;
02-DEC-1999;
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                                                                                                                                                                                                               AAU12355;
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AAU12172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bloactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing pro propagate, rectal, or live tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor alpha (TMF alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation of chondrocytes, the proliferation of funer ear utricular supporting cells or cartilage, the proliferation of funer ear utricular supporting cells or of T-lymphocytes, the release of a cytchine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the proliferation of endothelial cells. Some of the factor VIRA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The prolifers encoding proliferation of collections and proliferation of collections in proliferation of collections are supported to dentify the proliferation of encoding proliferation of collections in proliferations of a cyclosic or inhibit binding of A-peptide colles involved in binding interactions. The polypetides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   404
                                                                                                                                                                                                                                                                                                                                                                    transmembrane PRO polypeptide used to detect
link bioactive molecules to cells expressing
stect the presence of mammalian tumours e.g.
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Z;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QTCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPH
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100.0%; Pred. No. 2.4e-177;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12; Fig 368; 813pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             lung, breast, prostate, cervical
                                                                                                                                                                                                                                                                                                                                                            other PRO polypeptides, link round of tect
2000WO-US14941.
2000WO-US15264.
2000WO-US30873.
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                                                                                                                                                                                                     Goddard
                                                                                                                                                                           Beresini M,
                                                                                                                                                                                                                                   Stewart TA,
                                                                                                                     (GETH ) GENENTECH INC
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                                                                                                                                                                                                  Gerritsen ME,
Smith V, Stewa
                                                          10-NOV-2000;
30-MAY-2000;
02-JUN-2000;
                                                                                                                                                                           Baker KP,
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Query Match
Best Local Similarity
  when the chronic arthritis; special arthritis; systemic sclerosis; with the chronic arthritis; spondyloarthropathy; Sjogren's syndrome; Juvenile chronic arthritis; spondyloarthropathy; Sjogren's syndrome; diopathic inflammatory; myopathy; polymyosiths; systemic vasculitis; sarcoidosis; autoimmune haemolytic anaemia; immune pancytopaenia; thytoiditis; autoimmune thrombocytopaenia; idiopathic thrombocytopaenic purpura; thytoiditis; Grave's disease; Hashimoto's thytoiditis; diabetes mellitus; glomerulonephritis; demyelinating disease; multiple sclerosis; Guillain-Barre syndrome; hepatobiliary disease; who this manaetory demyelinating polymeuropathy; infectious hepatitis; who infammatory demyelinating polymeuropathy; infectious hepatitis; sclerosing cholangitis; ulcerative colitis; infammatory bowel disease; Crohn's disease; Whipple's disease;
Minflammatory bowel disease; Crohn's disease; Whipple's disease;
Minflammatory boxidasis; asthma; allergic rhinitis; urticaria; food hypersensitivity; eosinophilic pneumonia; graft rejection;
Milliomary fibrosis; graft versus-host-disease; immunogen;
          361 VLSDGTLNFTNVTVQDTGMYTCMVSNSVGNTTASATLNVTAATTTPFSYFSTVTVETMEP 420
                                       SQDEARTTDNNVGPTPVVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEV 478
                                                 183..187
/label= Phosphorylation_site
/note= "cAMP/cGMP dependent protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118..124
/note= "Glycine at 118 is N-myristoylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Glycine at 191 is N-myristoylated"
228..234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Glycine at 391 is N-myristoylated"
                                                                                                                                                                                               osteoarthritis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "Glycine is N-myristoylated"
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.e= "Asn is N-glycosylated"
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                                                                                                                                                                         Human immune response protein PRO331 (UNQ292).
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                                                                                                                                                                                             PRO331; UNQ292; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                              l..44
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                     5..640
| Tabel = Mature_PR0331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphorylation site"
191..197
                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                            AAU00826 standard; Protein; 640 AA.
                                                                                                                                                     (first entry)
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422..428
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                                                                                                                                                     04-JUL-2001
                                                                                                                                 AAU00826;
                                                                                                                                                                                                                                                                                                                                                             antibody.
                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
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The sequence responses Human FKO331 (unt221), a prouter involved in the sequence responses. PRO polypeptides, and (ant)agonists to them, are used in compositions for modulating infiltration of inflammatory cells into a tissue, modulating an immune response and modulating proliferation of T-lymphocytes in response to an antigen. Immune related diseases can of T-lymphocytes in response to an antigen. Immune related diseases can be treated with the compositions, such as, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthopathies, systemic sclerosis, idiopathic inflammatory myopathies (e.g. polymyositis), Sjoqren's syndrome, systemic vasculitis, arcoidosis, autoimmune haemolytic anaemia (e.g. immune pancytopaenia), cutoimmune thrombocytopaenia (e.g. idiopathic thrombocytopaenic purpura), thyroiditis (e.g. Grave's disease, Hashimoto's thyroiditis), diabetes cutoimmune thrombocytopaenia (e.g. idiopathic thrombocytopaenia correlated renal disease (e.g. glomerulonephritis), campliating diseases of the central and peripheral nervous systems e.g. cenyelinating polyneuropathy, hepatobiliary diseases such as infectious central and peripheral nervous systems. Ce hepatitis (hepatitis, A. B. C. D. E and other non-hepatotropic viruses), auto immune chronic active hepatitis, primary biliary cirrhosis, cutoimmune chronic active hepatitis, primary biliary cirrhosis, and colleis, cromine and Whipple's disease), and colleis, cromine and Whipple's disease), and colleis, cromine and whipple systems.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eosinophilic pneumonia, idiopathic pulmonary fibrosis, transplantation associated diseases including graft-versus-host-disease and graft rejection. PRO polypeptides can be used to diagnose immune related diseases, to identify inhibitors, and to stimulate the proliferation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents Human PRO331 (UNQ292), a protein involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition for diagnosing and treating immune related diseases, rheumatoid arthritis and diabetes mellitus, comprises a PRO polypeptide, agonist, antagonist or fragment -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune or immune-mediated skin diseases (e.g. erythaemia multiforme and psoriasis), asthma, allergic rhinitis, urticaria, food hypersensitivity, immunologic diseases of the lung such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hillan KJ, Tumas D,
                                                                                                                                                                                                                                                                                                                                                                                    531..537
/note= "Glycine is N-myristoylated"
606..610
/note= "Asn is N-glycosylated"
                             ...439 ...
te= "Glycine is N-myristoylated"
/note= "Glycine is N-myristoylated"
                                                                                               ...438
te= "Asn is N-glycosylated"
                                                                                                                                                                                                              "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                    "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                         /label= Transmembrane_domain 531..537
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                                                                                                                                                                             442..446
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Length 640;

Score 2524; DB 22; Pred. No. 2.4e-177;

100.0%; 100.0%;

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N-PSDB; AAF72423
                                                        Williams PM,
05-JAN-2000;
                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                               dermatological; antipsoriatic; cytostatic; antiinflammatory;
                                                                       180
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                                                                                                                                DLFTPLHHLERIHLHHNPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGEL 300
                                                                                                                                                            DQNYFTCYAPVIVEPPADLNVTEGMAAELKCRASTSLTSVSWITPNGTVMTHGAYKVRIA 360
                                                                                                                                                                                        VLSDGTLNFTNVTVQDTGMYTCMVSNSVGNTTASATLNVTAATTTPFSYFSTVTVETMEP 420
                     LQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIP 120
                                                  404
Gaps
            QTCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEI 60
                                                                               SYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDEL
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99US-0145698.
99US-0146222.
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99WO-US30999
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Conservative
                                                                                                                                                                                                                                                                                                                 Human PRO331 protein.
                                                                                                                                                                                                                                                                                                                                                                                              WO200104311-A1.
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                         22-FEB-2000;
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20-DEC-1999;
20-DEC-1999;
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Matches
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including
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                                                                                                                     Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QTCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEI
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                                                                                                                ME, Goddard
Kljavin IJ;
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                                                                                                                                                                 Tumas
                                                                                                                  H, Gerritsen M
Hillan KJ, K
Stewart TA,
                                                                                            Eaton DL,
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                                                                                            Desnoyers L,
V, Gerber H,
                                                                                          Ashkenazi AJ, Bousaca..., Gao W, Gerber H
Filvaroff E, Pong S, Gao W, Gurney AL,
Godowski PJ, Grimaldi CJ, Gurney AL,
Paoni NF, Roy MA,
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 104; 393pp; English.
99WO-US00219
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                                                                                                                                                              Pan J, Pac
, Wood WI;
                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                              Alzheimer's disease)
                                                                                                                                                                                                                                     WPI; 2001-081051/09
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Matches 478; Conserv
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(first entry)
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PJ;
                                                                                                       chromosomal mapping; gene mapping; tissue typing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Paoni NF;
Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, specific cells, to cause targeted cell death -
                                                                                             transmembrane protein; PRO; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gerber H, Gerritsen ME, Goddard A,
AL, Kljavin IJ, Napier MA, Pan J,
Tumas D, Watanabe CK, Williams PM,
                                                                          Human PRO331 protein sequence SEQ ID NO:501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Botstein D,
                 standard; Protein; 640 AA.
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99WO-US30095
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2000WO-US00376
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2000WO-US04341
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Grimaldi CJ, Gurney AL,
Roy MA, Stewart TA, Tumi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-032160/04.
                                                                                            secreted and
                                                                                                       cell death; cancer;
                                                                                                              diagnostic assay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAF44261
                                                                                                                                                    WO200073454-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                               11-FEB-2000;
18-FEB-2000;
22-FEB-2000;
                                                                                                                                  Homo sapiens
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28-JUL-1999
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                  AAB65292
                                    AAB65292;
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treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to AAB65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 DLFTPLHHLERIHLHNPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGEL 300
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                                                                                                                                                                                                                                                                                                                                                                                                        LQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIP 120
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                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QTCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEI
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                                                                                                                                                                                                                                                           Length 640;
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                                                                                                                                                                                                                                                           100.0%; Score 2524; DB 22; 100.0%; Pred. No. 2.4e-177;
                                                                                                                                                                                                                                                                                                                   0; Mismatches
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SYAFNRIPSTRRLDLGELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDEL

121

DLFTPLHHLERIHLHHNPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGEL

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181 DLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPH

LOLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIP 120

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9 οy g à g 300

344

DQNYFTCYAPVIVEPPADLNVTEGMAAELKCRASTSLTSVSWITPNGTVMTHGAYKVRIA 360

345 dqnyftcyapviveppadlnvtegmaaelkcrastsltsvswitpngtvmthgaykvria 404 VLSDGTLNFTNVTVQDTGMYTCMVSNSVGNTTASATLNVTAATTTPFSYFSTVTVETMEP 420

421 SQDEARTTDNNVGPTPVVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEV 478

465

284

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The invention relates to novel human anglogenesis-associated proteins designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding PRO proteins. The invention also relates to vectors and host cells . . . comprising a PRO nucleic acid, the recombinant production of a PRO protein, agonists of a RRO protein, agonists of a RRO protein, adonists of a PRO protein, and comprising a PRO protein, agonists or antagonists of a PRO protein, and comprising a PRO protein, adonists or a carlotvality; diagnosing of identifying modulators of PRO additionally encompasses methods of identifying modulators of PRO or activity; diagnosing of additionally encompasses methods of identifying modulators of PRO antagonist; a retroviral gene therapy vector comprising a particular tissue; treating a cardiovascular, endothelial or angiogenic disorder via the administration of a PRO protein, or stimulating endothelial or PRO nucleic acid; on moduced acid; and methods of inhibiting or stimulating endothelial cell growth, cardiac hypertrophy or PRO-induced angiogenist thereof. PRO nucleic acid; and methods of inhibiting or stimulating endothelial cell growth, cardiac hypertrophy or PRO-induced angiogenist thereof. PRO nucleic acids, PRO protein, or an agonist or antagonist thereof. PRO nucleic acids, proporteins, antibodies against PRO proteins, adherencelease, or stroke acids, myocadelal infarction, hypertension, diabetic retinopathy, rheumatoid arthritis, Crohn's disease, Huntington's disease, or stroke. PRO nucleic acids are additionally useful in the recombinant production of PRO proteins, and appeades encoding PRO proteins, a phybridisation probes to screen libraries to isolate cDNAs with sequence identity to PRO proteins, to map genes encoding PRO proteins, to map genes encoding PRO proteins, to map genes encoding PRO proteins, and processes encoding PRO proteins, to map genese encoding pro proteins and processes encoding properties, as hybridisa
                                                                                                                                                                                                                                                                                                                                                             Goddard A;
Mark MR, Marsters SA;
1, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid for producing a PRO polypeptide, analyzing genetic disorders and treating cardiovascular, endothelial or angiogenic disorders, such as atherosclerosis, wounds or cancer -
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AL, Hillan KJ, Kuo SS, Ma
Watanabe CK, Williams PM,
                                                                                                                                                                                                                                                                                                                                                               Baker KP, Ferrara N,
Jurney AL, Hillan KJ,
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99US-0144758
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                                         99WO-US12252
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                  99US-0134287
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                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
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                                                                                                                                         -SEP-1999;
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02-DEC-1999;
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                                         02-JUN-1999
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                                                                               20-JUL-1
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Human; leucine-rich repeat; LRR; 31939 protein; therapy; evel proliferation; differentiation disorder; denoce; neuronal disorder; neuronal disorder; neuronal disorder; denoce; neuronal disorder; denoce; neuronal disease; multiple sclerosis; degenerative disease; Alzheimer's disease; Huntington's disease; spinocerebellar degeneration; nervous system; bone disorder; osteoporosis; immune disorder; rheumatcoid arthritis; diabetes mellitus; cardiovascular disorder; theumatcoid arthritis; diabetes mellitus; cardiovascular disorder; theumatcoid arthritis; diabetes mellitus; cytostatic; nootropic; neuroprotective; anticonvulsant; osteopathic; antirheumatic; antiarthritic; virucide; analgesic.
                                                                                                     Human leucine-rich repeat (LRR) family member protein.
                                                                                                                                                                                                                                                                                                                                                                   "Mature human 31939 protein"
                                                                                                                                                                                                                                                                                                                                                                             56..85
/label- N-terminal_LRR_domain
87..110
                                                                                                                                                                                                                                                                                                                                       /label= Signal_peptide
                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                        AAE13006 standard; Protein; 713 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             135..158
/label= LRR_domain
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230..253
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                                                                             (first entry)
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                                                                             28-JAN-2002
                                                                                                                                                                                                                                                                                   sapiens
                                                   AAE13006;
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1 QTCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEI 60

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Gaps

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Indels

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0; Mismatches

Conservative

Query Match Best Local Similarity Matches 478; Conserv

100.0%; Score 2524; DB 22; Length 640; 100.0%; Pred. No. 2.4e-177;

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secreted protein; signal peptide; transmembrane domain; leucine zipper; hydrophobls nature; ToppredII computer program; cytokine; tissue growth; nutritional activity; cell proliferation; immune stimulation; chaoptin domain; immune suppression; hematopoiesis regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142..163
//label= Chaoptin_domain-3
/note= "Composed of 41 potentially amphipathic repeats"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Chaoptin_domain-2
/note= "Composed of 41 potentially amphipathic repeats"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261. 282
/label= Chaoptin_domain-4
/note= "Composed of 41 potentially amphipathic repeats"
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                          ONYFTCYAPVIVEPPADLNVTEGMAAELKCRASTSLTSVSWITPNGTVMTHGAYKVRIAV
                                                  ပဲ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone cc359_4; cc359_4 protein; human adult brain cDNA library;
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                                                                                                                             LSDGTLNFTNVTVQDTGMYTCMVSNSVGNTTASATLNVTAATTTP-----
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Steininger RJ;
                                                                                                                                                                                                                                  -----FSYFSTVTVETME--PSQD--EARTIDNN-VGPTPVVDW-
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                                                                                                                                                                                                                                                                                                                                  444 NVTTSLTPQSTRSTEKTFTIPVTDI-NSGIPGIDEV 478
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536 ssttapaprssrptekaftvpitdvtenalkdlddv 571
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Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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99US-0280591.
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Treacy M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptide useful for treating cancer, multiple sclerosis, Alzheimer's disease, osteoporosis, arthritis, and metabolic and liver disorders comprises the 31939 polypeptide belonging to the leucine-rich
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; Mismatches 74;
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                                                                                                                                                  C-terminal_LRR_domain
                                                                                                                                                                                                     /label= Immunoglobulin_domain
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ilarity 64.9%; Pred. No. 1.5e
Conservative 68; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Fig 1A-1C; 117pp; English.
                     254..277
/label= LRR_domain
/label= LRR_domain
                                                                                                  LRR_domain
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                                                                                               /label= Ll
311..362
/label= C
378..438
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N-PSDB; AAD21287.
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The present sequence is the cc359_4 secreted protein encoded by the cDNA clone cc359_4. cc359_4 was isolated from a human adult brain cDNA library using methods specific for secreted protein cDNAs. The leader sequence or signal peptide acts as a transmembrane domain due to its hydrophobic nature. The TopPredII computer program predicts five potential transmembrane domains centered around amino acids 20, 410, 490, 530 and 590. This protein has a leucine zipper motif. The polynucieotide and protein may effect nutrilional activity, cytokine and cell proliferation, immune stimulation or suppression, hematopoiesis regulation, tissue
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proliferation; tumourigenesis; identification; cancer; cytostatic; anootropic; neuroprotective; antiinflammatory; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                  LOLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIP 120
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brain, human fetal brain, human fetal kidney, and human adult
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                                                                                                                                                                                                                                                                                                                  DB 20; Length 653;
                                                                                                                                                                                                                                                                                                              Similarity 62.7%; Score 1581.5; DB 20; Lengt Similarity 60.9%; Pred. No. 5.1e-108; Onservative 77; Mismatches 93; Indels
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                                                 Claim 1; Page 97-99; 122pp; English.
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                 CDNA libraries
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                                                                                                                                                                                                                                                                653 AA;
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Matches 298; C
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blood
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The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PR0212, PR030, PR0341, PR0515, PR0619, PR0717, PR08107, PR08107, PR09111, PR0105, PR01009, PR01081, PR01035, PR01035, PR01035, PR01035, PR01035, PR01031, PR01181, PR01181, PR01218, PR02198, PR02198, PR02198, PR02198, PR02198, PR03198, PR
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immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; neuronal disorder; gilal disorder; astrocytal disorder; angiogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immunologic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hillan KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptides, useful cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thirty PRO polynucleotides encoding treatment, diagnosis and prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 61; Fig 34; 286pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US28313.
99WO-US30911.
2000WO-US00219.
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99US-0141037.
99US-0143048.
99US-0145698.
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                                                                                                                                 Homo sapiens.
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05-JAN-2000;
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10 - JUN - 1998;
11 - JUN - 1998;
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17-JUN-1998;
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  Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand; pharmaceutical; receptor immunoadhesin; gene mapping.
                  SYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDEL 180
                                                              DLFTPLHHLERIHLHHNPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGEL 300
                                                                                               VLSDGTLNFTNVTVQDTGMYTCMVSNSVGNTTASATLNVTAA--TTTPFSYFSTVTVETM 418
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                           DLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPH 240
                                                                                                                         DQNYFTCYAPVIVEPPADLNVTEGMAAELKCRASTSLTSVSWITPNGTVMTHGAYKVRIA 360
104 lqlgrnsirqievgafnglaslntlelfdnwltvipsgafeylsklrelwlrnnpiesip 163
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DB 21; Length 653;

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are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Watanabe CK;
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Yuan J;
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Wood WI,
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Human; Alzheimer's disease; amyotrophic lateral sclerosis; ALS; Zollinger-Ellison syndrome; immune system disease; schizophrenia; inflammation; haematopoietic disease; anxiety; feeding disorder; aging; anorexia; depression; cardiovascular disease; sleep disorder; selaure; memory alteration; migraine; stroke; asthma; neuropathy; hypoglycaemia; sexual disorder; growth abnormality; infection; autoimmune disease; rheunatoid arthritis; cataractogenesis; anglogenesis; atherosclerosis; crebral ischaemia; cirrhosis; Huntington's disease; Hodgson's disease; hypercholesterolaemia; heddache; annesla; cardiac arrhythmia; obesity; cancer; vaccine; gene therapy; sbgPRO331a gene.
                                                                     LQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIP 120
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                                                       1 QTCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEI 60
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62.7%; Score 1581.5; DB : 60.9%; Pred. No. 5.1e-108 :ive 77; Mismatches 93
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The present sequence is a numbrane associated polypeptides.

The invention relates to secreted and membrane associated polypeptides.

The invention relates to secreted and membrane associated polypeptides.

The invention are useful for treating diseases such as Alzheimer's disease, invention are useful for treating diseases such as Alzheimer's disease, amyotrophic lateral sclerosis (ALS), Zollinger-Ellison syndrome, diseases of the immune system, haematopoletic disease, inflammation, anxiety.

Cof the inmune system, neoropathy, aging, sexual disorder, learning and memory alteration and altered immune response, selzure, migraine, cancer, stroke, asthma, neuropathy, aging, sexual disorders, treatment of transsexuals, growth abnormalities, obesity, infections, autoimmune of transsexuals, growth abnormalities, obesity, infections, autoimmune cancer, stroke, asthma, neuropathy, aging, sexual disorders, treatment of transsexuals, growth abnormalities, obesity, infections, autoimmune cof diseases (e.g. rheumatoid arthritis), cataractogenesis, angiogenesis, disorders associated with healthy maintenance of gastric mucosa and crepair of acute and chronic mucosal lesion, lung carcinoma, cerebral cischeamia, atherosclerosis, Girhosis, Huntington's disease, headache, ammesia, multiple sclerosis, Girhosis, Huntington's disease, headache, congestive heart failure, cardiac arrhythmias, hypercholesterolaemia, viral and non viral hepatitis, type I and type II diabetes mellitus, congestive heart failure, cardiac arrhythmias, hypercholesterolaemia, plommerulonephritis and malignant hyperthemia. Polypeptides of the invention are used to identify membrane bound and soluble receptors. They are also useful as vaccines for inducing an immunological response.

They are also useful as vaccines for inducing an immunological response.
                                                                                                                                                                                                                                                                                          New secreted and membrane associated polypeptides for treating Alzheimer's disease, psoriasis, cancer, enterocolitis, sleep and sexual disorders, stroke, and asthma
                                                                                                                                                               Xiang Z;
                                                                                                                                                               Smith RF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a human sbgPRO331a protein,
                                                                                                                                                               Rizvi SK,
                                                                                                                                                            Murdoch PR,
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 56-58; 94pp; English.
                                                                           (SMIK ) SMITHKLINE BEECHAM CORP.
18-APR-2000; 2000US-0198583. 04-OCT-2000; 2000US-0237963.
                                                                                                                                                            Kabnick KS,
                                                                                                                                                                                                            WPI; 2001-536566/59.
N-PSDB; AAD16345.
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                                                                  SYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDEL 180
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                              21; Gaps
                                                     1 QTCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEI 60
     Length 653;
                              93; Indels
   DB 22;
  Score 1581.5; DB 2:
Pred. No. 5.1e-108;
7; Mismatches 93;
62.7%; Scor
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Best Local Similarity 60.99
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Page 16

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Copyright (c) 1993 - 2000 Compugen Ltd
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283138

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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222 LOSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHNPWNCNCDILWLSWWIKDMAPSNTA 281

342 WITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGNTTASATLNVTA 401

282 CCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAELKCRASTSLTSVS 341

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131 VDPVAAGGTGSGGGGGGGGGGGGGGGTYFTTVTVETLETQPGEEALQPRGTEKEPPG 434 PTPVVDW------ETTNVTTSLTPQSTRSTEKTFTIPVTDI-NSGIPGIDEV 478

glial cell membrane glycoprotein LIG-1 precursor - mouse C;Species: Mus musculus (house mouse)

MEGF5 protein - ra slit protein 2 pre slit protein 1 pre hypothetical prote peroxidasin - frui insulin-like growt insulin-like growt hypothetical prote hypothetical prote gene wheeler prote hypothetical prote slit-1 protein ĥom MEGF5 protein - ra lysine carboxypept neuronal leucine-r chondroadherin pre secreted leucine-r insulin-like growt glycoprot insulin-like growt oncofetal trophobl platelet membrane decorin precursor decorin precursor decorin precursor decorin precursor platelet qlycopro decorin precursor decorin - rabbit Description SUMMARIES S46224 JC1282 JC6128 NBHUC8 S06280 147020 A34901 746266 A58532 JC7763 A53860 T42218 T13953 B36665 T28715 T42626 A60164 JC5239 A55454 441915 123841 529145 Query Match Length DB 789 1355 1025 560 605 1535 1151.5 402.5 290.5 286.5 286.5 286.5 283.5 283.5 283.5 281.5 Score 394 389.5 365.5 344.5 329.5 329.5 314.5 313 302.5 302.5 293 396 Result No.

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JE0176 JG01887 JG01887 JG01993 S20811 S20811 J125194 T129341 T119939 T115864 T129972 I139068	ÁLIG 9.1 - hu vision O s, H.W.; e Databa 1 gdala; c	Sco Pre
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT T46.266 hypothetical protein DKFZp761A179.1 - h C; Species: Homo sapiens (man) C; Date: 04-Feb-2000 #sequence_revision C; Accession: T46.56 R; Blum, H.; Bauersachs, S.; Mewes, H.W. submitted to the Protein Sequence Datab A; Reference number: Z23034 A; Reference number: Z23034 A; Accession: T46.26 A; Status: preliminary A; Accession: T46.20 A; Residues: 1-421 A; Residues: Breimental source: adult amygdala; C; Genetics: A; Note: DKFZp761A179.1	Query Match Best Local Matches 21

723 TPRITWLKGGRPLSLT 738

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C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Datession: JC7763
S;Fukamachi, K; Matsuoka, Y; Kitanaka, C.; Kuchino, Y.; Tsuda, H.
Biochem. Biophys. Res. Commun. 287, 257-263, 2001
A;Title: Rat neuronal leucine-rich repeat protein-3: Cloning and regulation of the ge A;Contents: Fibrosarcoma cells
                                                                                                                                                                                                                                                                                                                                                               C;Comment: This protein, a new member of the neuronal leucine-rich repeat protein fam in protein-protein interaction and functions as a cell adhesion molecule or soluble 1
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N;Alternate names: 38K leucine-rich protein
C;Species: Bos primigenius taurus (cattle)
C;Date: 07-oct-1994 #sequence_revision 07-oct-1994 #text_change 05-Nov-1999
C;Accession: A53860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---NLTPLIKLDE-----LDL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FMEPDSLFCV----DPPEFQGQNVRQVHFRDMMEICLPLIAPESFPSILDVEADSYVSLH 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 HNLLSAISPGAFVGLHNLRLHLHSNRLQMINSKWFEALPNLEILMLGD-NPILRIKDMN 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --QIQVIER 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHNPWNCNCDILWLSW---WIK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DMAPSNTACCARCNTPPNLKGRYIGELD-QNYFTCYAPVIVEP--PADLNVTEGMAAELK 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -------VNSFKHLRHLEILQLSR------NHIRTIEIGAFNGLANLNTLELF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 CPQLCTCEIRPWFTPRSIYMEASTVDCNDLGLLNFPARLPADTQILLLQTNNIARIEHST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.7%; Score 396; DB 2; Length 70
25.9%; Pred. No. 1.2e-19;
Live 79; Mismatches 186; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---IQS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 SGNHLSAIRPGSFQGLMHLQKLWM----
                                                                                                       neuronal leucine-rich repeat protein-3
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                                                                                                                                                                                                                                                                                  A; Accession: JC7763
A; Molecule type: mRNA
A; Residues: 1-707 cFUK>
A; Cross-references: GB: AF291437
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Best Local Similarity 25.9%
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Keywords: cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       504 ADLKSIMIKV 513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 CPSVCSCS----
                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: nlrr-3
                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
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                                         R.Suzuki, Y.; Sato, N.; Tohyama, M.; Wanaka, A.; Takagi, T.
J. Biol. Chem. 271, 22522-22527, 1996
A;Title: CDNA cloning of a novel membrane glycoprotein that is expressed specifically A;Reference number: A58532; MUID:96394313
A;Accession: A58532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
C:Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 05-Nov-1999 C;Accession: A58532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MVSNSVGNTTASATLNVTAATTTPFSYFSTVTVETMEPSQDEARTTDNNV-----GP 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGSLYGLTALHQLHLSNNSISRIQRDGWSFCQKLHELILSFNNLTRLDEESLAELSSLSI 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDELDLSGNHLSAIRPG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AFTGLDNLSKLTLFGNKIKSVAKRAFSGLESLEHLNLGENAIRSVQFDAFAKMKNLKELY 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254 LHHNPWNCNCDILWLSWWI--KDMAPSNTACCARCNTPPNLKGRYI-GELDQNY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 15.9%; Score 402.5; DB 2; Best Local Similarity 24.1%; Pred. No. 7.5e-20; Matches 134; Conservative 77; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --FTCYA---
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Allernate names: slit protein homolog
C; Species: Rattus norvegicus (Norway rat)
C; Accession: T13959
R; Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A; Title: Identification of high-molecular-weight proteins with multiple EGF-like moti
A; Reference number: Z14126; MUID:98360089
A; Reference number: Z14126; MUID:98360089
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-1523 < NAK>
A; Residues: 1-1533 < NAK>
A; C; Genetics:
A; Ge
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                                                                                                                         LDLGEL---KRLSYISE----- GAF---EGLSNLRYLNL---------------------160
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     | | | : | |||:
LMENQIGAVERGAFDDMKELERLRLNRNQLQVLPELLFQNNQALSRLDLSENSLQAVPRK 151
                                                                                                                                                                                                                                                              LHSNHLFCDCHLAWLSQWLRQRPTIGLFTQCSGPASLRGLNVAEVQKSEFSCSGQGEAAQ 271
                                                                                                                                                                                                                                                                                                                       -----LREIP--NLTP 173
                                                                                                                                                                                                                                                                                                                                                             DFLRTNPIETTG -- ARCASPRRLANKRIGQIKSKKFRCSAKEQYFIPGTEDYHLNSECTS 509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---GLANLNTLELFONRLTTPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLR--R
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                                                                                                                                                                                                                                                                                                                       324 GMAAELKCRASTSLTSVS 341
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Matches 115; Conservative
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                                                                                                       A; Accession: A53860
A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-361 <NEA>
A; Cross-references: GB:U08018; NID:9470671; PIDN:AAA21330.1; PID:9470672
C; Superfamily: leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan carboxyl-C; Keywords: disulfide bond
E; 300-346/Domain: proteoglycan carboxyl-terminal homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NiAlternate names: MEGF4 protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 0.2 Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C;Accession: T42218
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A;Reference number: 214126; MUID:98360089
R;Neame, P.J.; Sommarin, Y.; Boynton, R.E.; Heinegard, D.
1. Biol. Chem. 269, 1254-21354, 1994
A;Title: The structure of a 38-kDa leucine-rich protein (chondroadherin) isolated from A;Reference number: A53860; MUID:94342341
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A;Molecule type: mRNA
A;Residues: 1-1531 <NAK.
A;Cross-references: EMBL.AB011530; NID:93449289; PIDN:BAA32460.1; PID:93449290
A;Experimental source: strain Sprague-Dawley; brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 LLSPLVNLFILQLNNNKIRELRSGAFQGAKDLRWLYLSE-NSLSSLQPGALDDVENLAKF 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLAMCNLREIPN--LTPLIKLDELDLSGNHLSAIRPGSFQGL-MHLQKLWMIQSQIQVIE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 YLDRNQLSSYPSAALSKLRYVVEELKISHNPLKSIPDNAFQSFGRYLETIMLDNTNLEKFS 262
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                                                                                                                                                                                                                                                                                                                                                                                                 15.6%; Score 394; DB 2; Length 361; 31.9%; Pred. No. 6.9e-20; tive 49; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Pred. No. 9.3e-19;
5; Mismatches 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: Z14126; MUID: 98360089
A; Accession: T42218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      276 APSNTACCARCNTPPNLKGRYIGELD 301
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24.9%;
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Best Local Similarity
Matches 104; Conserv
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A; Experimental
C; Genetics:
A; Gene: MEGF4
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Qy 211 IQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNCDILMLSW 270	OY 167 166 DD 471 PIETSGARCESPKRMHRRRIESLREEKFKCSWGELRMKLSGECRMDSDCPAMCHCEGTTV 530
QY 271 WIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTC 307 ::: : :	QY 167EIDLSAIRPGS 194 1
BESULT 7 B36655 B3665 B36655 B	OY 195 FOGLMHLOKLWMIOSOIOVIERNAFDNLQSLVEINLAHNNLTLLPHDLETPLHHLERIHL 254
	RESULT 8 A36665 Slit protein 1 precursor - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 17-Nov-2000 C;Accession: A36665; A31640; S13523
-2-glycc	R;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S. Genes Dev. 4, 2169-2187, 1990 A;Title: an extracellular protein necessary for development of midline glia and A;Reference number: A36665; MUID:91099665 A;Accession: A36665
	A;Status: preliminary A;Molecule type: mRNA A;Moscule type: mRNA A;Residues: 1-1480 cR0T> A;Residues: 1-1480 cR0T> A;Cross-references: GB:X53959; NID:g8614; PIDN:CAA37910.1; PID:g8615 A;Cross-references: GB:X53959; NID:g8614; PIDN:CAA37910.1; PID:g8615 Ccll 55, 1047-1059, 1988
	A; Title: Slit: An EGF-homologous locus of D. melanogaster involved in the development A; Reference number: A31640; MUID:89077533 A; Accession: A31640 A; Molecule type: DMA A; Mesulues: 881-1182, 'G', 1185-1404, 'GT', 1463-1464, 'YHA' <r02> A; Cross-references: GB:M23543; NID:g340939; PID:g514357</r02>
	C:Genetics: A;Gene: FlyBase:Sli A;Cross-references: FlyBase:FBgn0003425 A;Introps: 1331,33 A;Introps: 1331,33 A;Introps: FlyBase:FBgn0003425 A;Introps: 1331,33 A;Int
Query Match 13.9%; Score 350; DB 2; Length 1469; Best Local Similarity 23.9%; Pred: No. 4.8e-16; Matches 109; Conservative 65; Mismatches 152; Indels 130; Gaps 9;	F;197-12/Obmain: recurrering alpha 2-91/Coprocent repeat nonology CLAND. F;228-272/Domain: proteoglycan carboxyl-terminal homology <pcsi> F;228-313/Domain: proteoglycan amino-terminal homology <pah2> F;238-346/Domain: leucing-rich alpha-2-91/coprotein repeat homology <lrr6> F;347-370/Domain: leucing-rich alpha-2-91/coprotein repeat homology <lrr7> F;371-394/Domain: leucing-rich alpha-2-91/coprotein repeat homology <lrr7></lrr7></lrr7></lrr6></pah2></pcsi>
Qy 2 TCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEIL 61 11 1 1 1 1 1 1 1 1	F;395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <lrr9> F;419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <lr10> F;450-494/Domain: proteoglycan carboxyl-terminal homology <pcs2> F;512-537/Domain: proteoglycan amino-terminal homology <pr3> F;512-537/Domain: leucine-rich alpha-2-glycoprotein repeat homology <lr11></lr11></pr3></pcs2></lr10></lrr9>

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CESP: T21D12.9a
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A;Introns: 38/2; 84/2; 132/2; 204/2; 275/2; 351/2; 519/3; 615/1; 714/1; 758/2
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C;Species: Ceenorhabditis elegans
C;Date: 15-Oct-1999 *sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T28714
                                                                                                                                <LR15>
<LR16>
       <LR12>
<LR13>
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                                                         <LR14>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 QLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------EIPNLTPL------IKLD-------ELDLSGNHLSAIRPGS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 TCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEIL
F;572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology < F;596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology < F;620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology < F;621-695/Domain: proteoglycan carboxyl-terminal homology < PCS3> F;708-733/Domain: proteoglycan amino-terminal homology < PCS3> F;743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology < F;767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology < F;815-838/Domain: leucine-rich alpha-2-glycoprotein repeat homology < F;815-838/Domain: proteoglycan carboxyl-terminal homology < F;1028-1061/Domain: EGF homology < EGF> F;1088-1099/Domain: EGF homology < EGF> F;1058-1099/Domain: EGF homology < EGF> F;115-1148/Domain: EGF homology < EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                      152; Indels 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-789 <WOE>
A;Cross-references: EMBL:AF016687; PIDN:AAC48096.1; GSPDB:GN00022;
A;Experimental source: strain Bristol N2; clone T21D12
                                                                                                                                                                                                                                                                                                                                                                                    Length 1480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 YAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAM-----CNLR----
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                                                                                                                                                                                                                                                                                                                                                                                 13.9%; Score 350; DB 2; 23.9%; Pred. No. 4.8e-16; iive 65; Mismatches 152
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A;Molecule type: DNA
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Introns: 38/2; 84/2; 132/2; 204/2; 275/2; 351/2; 519/3; 615/1; 714/1; 758/2; 786/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
**Residues: 1-1355 CWDE.>
A;Residues: 1-1355 CWDE.>
A;Cross-references: EMBL.AF016687; PIDN:AAC48095.1; GSPDB:GN00022; CESP:T21D12.9b
A;Experimental source: strain Bristol N2; clone T21D12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein T21D12.9b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T28715
R;Woessner, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 GNHLS-AIRPGSF---QGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLP 239
                                                                                                                                                                                                                      161 NDVYRLDDGMFYACEGLKHLNLSTNRVQAVTEGWMFGLTSLEVLDLSYNQIQSFHISSWS 220
                                                                                                                                                                                                                                                                                                                                                                   239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --PSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPN--LTPLIKLDELDLS 183
                                                                                                                              240 HDLFTPLHHLERIHLHHNPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGE 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STNTRL-LNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFD 89
                                                                                                                                                                                                                                                                                                                                                                   184 GNHLS-AIRPGSF---QGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLP
                                                                                                                                                                                                                                                                                                                                                                                              280 SNTLAVCVEDGAVLYNTSMPFLRSLRFTNNQLRVIPKRAFERFPALEELDLTDNPIATIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :| ||: | |: | |: | | |: | | |: | | | |: | | | |: | | | |: | | | |: | | | |: | | | |: | | | |: | | | | |: | | |
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                                                                                                31 STNTRL-LNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFD
                                                                                                                                                                                                                                                                             --PSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPN--LTPLIKLDELDLS
                                                                                                                                                                                                                                                                                                                     221 HTPKLKWLSL-HSNRIQSLPSGSFRVLRQLEELILSANSIDSLHKFALVGMSSLHKLDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221 HTPKLKWLSL-HSNRIQSLPSGSFRVLRQLEELILSANSIDSLHKFALVGMSSLHKLDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 LDQNYFTCY----APVIVEPPADLNVTEGMAAELKCRA-STSLTSVSW------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343 -----ITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGN 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 459 QDSATFLSINRTAVVNGTFDER--ELAAAELLLDNVAMTDNSEYQCVARNRFGS 510
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                                                       58;
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                                                                                                                                                                                          ---SYAFNRI---
             Length 789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SYAFNRI-
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, August 1997
A; Description: The sequence of C. elegans cosmid T21D12.
A; Reference number: 220514
A; Accession: T28715
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                      90 NRLTTIPNGAFVYLSKLKELWLRNNPIESIP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NRLTTIPNGAFVYLSKLKELWLRNNPIESIP--
                             Similarity 26.3:
09; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 109; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: CESP:T21D12.9b
           Query Match
Best Local Simi
Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Genetics:
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A; Molecule type: protein A; Molecule type: protein A; Molecule type: protein A; Residues: 477-478(, Fx', 481-485, E', 487, 'V', 489-492, 'NQ', 495, 'E', 497-498 <ZAF> A; Residues: 477-478(, F.S.; Yagi, M.; Roth, G.J. Proc. Nall. Acad. Sci. U.S. A. 90, 8327-8331, 1993 A; Title: Human platelet glycoprotein V: characterization of the polypeptide and the r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A;Residues: 252-266, H',268-272, X',274-279, I',281-284, I',286 <R03>
A;Residues: 252-266, H',268-272, X',274-279, I',281-284, I',286 <R03>
A;Note: this proteolytic fragment was designated peptide M401
R;Zafar, R.S.; Walz, D.A.
Thromb. Res. 53, 31-44, 1989
A;Title: Platelet membrane glycoprotein V: characterization of the thrombin-sensitive A;Reference number: A60432; MUID:89162331
C;Date: 12-Jan-1993 #sequence_revision 24-Feb-1994 #text_change 05-Nov-1999
C;Accession: A46030; A50164; A35483; B35483; A60423; A47507; S34329
R;Lanza, F.; Morales, M.; de La Salle, C.; Cazenave, J.P.; Clemetson, K.J.; Shlmomura
J. Biol. Chem. 268, 20801-20807, 1993
A;Title: Cloning and characterization of the gene encoding the human platelet glycopr
A;Reference number: A48030; MUID:94012616
                                                                                                                                                                                                                           A;Cross-references: EMBL:223091; NID:9312501; PIDN:CAA80637.1; PID:9312502
R;Shimomura, T.; Fujimura, K.; Maehama, S.; Takemoto, M.; Oda, K.; Fujimoto, T.; Oyam
Blood 75, 2349-2356, 1990
A;Title: Rapid purification and characterization of human platelet glycoprotein V: th
A;Reference number: A60164; MUID:90275263
                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 5pter-5qter
C;Superfamily: leucine-rich alpha-2-glycoprotein repeat homology
C;Keywords: blocked amino end; glycoprotein; platelet; tandem repeat; transmembrane p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contain two peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLTHLPKGLLGAQAKLERLLLHSNRLVSLDSGLLNSLGALTELQFHRNHIRSIAPGAFDR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNN 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Cross-references: GB:L11238, NID:g388759, PIDN:AAA03069.1; PID:g388760 C;Comment: This platelet membrane protein is a substrate for thrombin. C;Comment: The amino end of the intact protein is blocked. C;Comment: This protein is absent in Bernard-Soulier syndrome. C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---ISTNTRLLN------LHENQIQIIKVNSFKH
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A; Residues: 145-166, I', 168-169, X', 171-172 <ROT>
A; Note: this proteclytic fragment was designated peptide
A; Accession: B35483
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nes 104;
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A;Residues: 121-129, W',131-135;466-468,'X',470 <RO2>
A;Note: this material was designated peptide M393 but
A;Accession: C35483
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29.7%; Pred. No. 3.5e
ive 43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GDB:230236; OMIM:173511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A47507; MUID:93391348
A; Accession: A47507
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Best Local Similarity 29.77
Matches 83; Conservative
                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-560 <LA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-560 <RES>
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R:Holmes, G.P.; Negus, K.; Burridge, L.; Raman, S.; Algar, E.; Yamada, T.; Little, M.H.
Mech. Dev. 79, 57-72, 1998
A;Title: Distinct but overlapping expression patterns of two vertebrate slit homologs in
A;Reference number: 222177; MUID:99279238
A;Accession: T42626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIDN: AAD04345.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      secreted leucine-rich repeat-containing protein SLIT2 - mouse (fragment)
N;Alternate names: neurogenic extracellular slit protein
C;Species: Mus musculus (house mouse)
C;Species: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
  342
                                                                                                                                                                                                                                458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDCNMQWLSDWVK--SEYKEPGIARCAGPGEMADKLLTTPSKKFTCQGPMDITIQAKCN 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 QLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---LDELDLSGNHLSAIRPGSFQGLMH 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHNPWN 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLN 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 CPEKCRCEG--TTVDCSNQRLNKIPDHIPQYTAELRLNNNEFTVLEATGIFKKLPQLRXI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNS-FKHLRHLEİL 61
                                                                            HDLFTPLHHLERIHLHHNPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGE
                                                                                                                                                                                                              239 KGLKVLPKGIPKDVTELYLDGNQFTLVPKELSNYKHUTLIDLSNNRISTLSNQXFSNNTQ
                                                                                                                                                                              LDQNYFTCY----APVIVEPPADLNVTEGMAAELKCRA-STSLTSVSW------
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                                                                                                                                                                                                                                                                                  ----ITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGN 390
                                                                                                                                                                                                                                                                                                             459 QDSATFLSINRTAVVNGTFDER--ELAAAELLLDNVAMTDNSEYQCVARNRFGS 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1025;
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A;Cross-references: EMBL:AF074960; NID:g4151258; PID:g4151259;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAM----CN----
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larity 24.3%; Pred. No. 7.1e-16;
Conservative 62; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: mRNA
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Best Local Similarity
Matches 102; Conserv
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NyAlternate names: Acid-Labile Subunit (ALS)
C; Species: Homo sapiens (man)
C; Species: Homo 
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                                                                                      insulin-like growth factor-binding complex acid-labile chain precursor - human
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C;Species: Drosophila sp.
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Oct-2000
C;Accession: S46224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 TIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <LRR3>
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                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GB: M86826; NID: 9184807; PIDN: AAA36047.1; PID: 9184808
                                                                                                                                                                                                                                                                                                                                                                                         154 NLRYLNLAMCNLREIPN--LTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 QVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHN 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.5%; Score 314.5; DB 2; 31.1%; Pred. No. 4.3e-14; ive 47; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                protein
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                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA; F
A;Residues: 1-605 <LEO>
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Best Local S
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                                                                                                                 344 -----LALHSNGLTALPDGLLRGLGKLRQVSLRRNRLRALPRALFRNLSSLESVQLDHNQ 398**
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115 PIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPNLTPL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             460 LEYLLLSHNRLAELPADALGPLORAFWLDVSHNRLEALPGSLLASLGRLRYLNLRNNSLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 AIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269;
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                         13.1%; Score 329.5; DB 2; 21.0%; Pred. No. 3.9e-15; tive 61; Mismatches 118;
                                                                                                                                                                                                 235 LTLLPHDLFTPLHHLERIHLHHNPWNCNCDILWLSWWIK 273
                                                                                                                                                                                                                                                                                                                         insulin-like growth factor acid-labile chain - baboon
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Best Local Similarity 21.0%
Matches 119; Conservative
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R;Nelson, R.E.; Fessler, L.I.; Takagi, Y.; Blumberg, B.; Keene, D.R.; Olson, P.F.; Parke EMBO J. 13, 3438-3447, 1994
A;Title: Peroxidasin: a novel enzyme-matrix protein of Drosophila development.
A;Reference number: $46224; MUID:94341255
A;Accession: $46224
                                                                                                                                              A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1535 <NEL>
A;Residues: 1-1535 <NEL>
Cross-references: GB:U11052; NID:g531384; PIDN:AAA61568.1; PID:g531385
C;Superfamily: peroxidasin; myeloperoxidase homology; proteoglycan amino-terminal homology
F;19-44/Domain: proteoglycan amino-terminal homology <PAH4>
F;661-1350/Domain: myeloperoxidase homology <MPX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 AFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDELDL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 SGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDL 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 FTPLHHLERIHLHHN--PWNCNCDI--LMLSWWIKDMAPSNTACCARCNTPPNLKGRYIG 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 FNRLNNLKRLRLDGNAIDIDCNCGVYSLWRRWHL-DVQRQLVSISLTCAAPQMLQNQGFS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 SLGEHHFKCAKPQFLVAPQDAQVAAGEQVELSCEV-TGLHRPQITWM--HNTQELGLEEQ 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 LSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 -------NDIWQLPAGL-----FDNLPRLNRLIMYNNKLTQLPVDG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299 ELDQNYFTCYAPVIVEPPADLNVTEGMAAELKCRASTSL - TSVSWITPNGTVMTHGAYK 356
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
12.4%; Score 313; DB 2; Length 1535;
Best Local Similarity 24.7%; Pred. No. 1.8e-13;
Matches 97; Conservative 52; Mismatches 136; Indels 108; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 CPAGCTCLER--TVRCIRAKLSAVP-------KLPQDIQTLD 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQ 62
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094933 P51888 015455 062702 035103 P12024 060938 P23515 Q63912

homo sapien homo sapien mus musculu

mus musculu homo sapien

Sequence:

Run on:

Searched:

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Oncogene 16:2997-3002(1998).

--- SUBCELLUIGAR LOCATION: Type I membrane protein (Potential).

--- SINGLARITY: OVERAMPLIFIED IN MALIGNANT GLIOMAS.

--- SIMILARITY: DELONGS TO THE INMUNOGLOBULIN SUPERRAMILY.

--- SIMILARITY: CONTAINS 1 ILMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

--- SIMILARITY: CONTAINS 1 ILMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

--- SIMILARITY: CONTAINS 1 LEUCINE-RICH REPEATS (LRR).

--- SIMILARITY: CONTAINS 1 LEUCINE-RICH REPEATS (LRR).

--- THE SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98324709; PubMed=9662332; Malfory B., Almeida A., Zhu X.X., Vogt N., Tyagi R., Muleris M., Malfoy B., Almeida A., Zhu X.X., Vogt N., Tyagi R., Muleris M., Dutrillaux A.-M., Dutrillaux B., Ross D., Hanash S.; "GACI, a new member of the leucine-rich repeat superfamily on chromosome band 1q32.1, is amplified and overexpressed in malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_raxID=9606;
                                                                                                                                                                                                                                                                                                                                                                16-077-2001 (Rel. 40, Created)
16-077-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Glioma amplified on chromosome 1 protein precursor.
                                                                                                                                                                                                                                                                                                                                 713 AA
                                                                                                                                                                                                                                             ALIGNMENTS
                TLR3_MOUSE
Y848_HUMAN
PRLP_HUMAN
TLR3_HUMAN
TERA_BOVIN
OMD_MOUSE
CHAO_DROME
                                                                                                                                        KERA_HUMAN
                                                                                                                                                        OMGP_HUMAN
                                                                                                                                                                          CHAO_TRICA
                                                                                                                                                                                           SMGP MOUSE
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InterPro; IPR003598; Ig_c2.
InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR_Cterm.
InterPro; IPR000372; LRR_NETERM.
InterPro; IPR003592; LRR_Out.
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MIM; 605492; -.
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Pfam; PF01462; LRRNT; 1.
PRINTS; PR00019; LEURICHRPT.
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SM00370; LRR; 6.
SM00082; LRRCT; 1.
SM00013; LRRNT; 1.
SM00369; LRR_TYP; 2
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Pfam; PF00560; LRR; 10.
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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SLIT_DROME
GPV_HUMAN
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PGS1_HORSE
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Match Length DB
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Result Š

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Bos taurus (Bovine).
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01-NOV-1997
           CHAD_BOVIN
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                             CHROMOSOME 1 PROTEIN.
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NKNPLORVGPGDFANMLHLKELGLNNMEELVSIDKFALVNLPELTKLDITNNPRLSFIHP 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            445
                                                                                                                                                                                                                                                                                                                                      52 FKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWL 111
                                                                                                                                                                                                                                                         17.1%; Score 430.5; DB 1; Length 713;
25.1%; Pred. No. 2.9e-23;
1ve 83; Mismatches 211; Indels 123; Gaps
                                                                                                                                                                                                                                                                                                CPSVCSCS------NQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNS 51
                                                                                                                                                                                                                                                                                                                   CPPQCACQIRPWYTPRSSYREATTVDCNDLFLTAVPPALPAGTQTLLLQSNSIVRVDQSE 88
                                                                                                                                                           LER 11.

IG-LIKE C2-TYPE DOMAIN.

BY SIMILARITY.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                       389 FIEPQSTLCA----EPPDLGRLPVREVPFREMTDHCLPLISPRSFPSLQVASGESMVLH
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Immunoglobulin domain; Transmembrane; Glycoprotein; Repeat;
                            GLIOMA AMPLIFIED ON CHROMO:
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                               EC8BC0FD240C9396 CRC64;
                                                         CYTOPLASMIC (POTENTIAL).
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Best Local Simil
Matches 140; (
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                                                                                                                        Chondroadherin precursor (Cartilage leucine-rich protein) (38 kDa bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEATS
                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein (chondroadherin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hu B., Coulson L., Moyer B., Price P.A.; "Isolation and molecular cloning of a novel bone phosphoprotein related in sequence to the cystatin family of thiol protease inhibitors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHONDROADHERIN.
CHONDROADHERIN, MINOR FORM.
10 X 24 AA LEUCINE-RICH TANDEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 (IN SOME ISOFORM(S)).
                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Cartilage,
MEDLINE-94342341; PubMed-8063792;
Neame P.J., Sommarin Y., Boynton R.E., Heinegaard D.;
"The structure of a 38-kDa leucine-rich protein (chond isolated from bovine cartilage.";
J. Biol. Chem. 269:21547-21554(1994).
                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REF.
REF.
361 AA
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PRT;
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InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR.Cterm.
InterPro; IPR000372; LRR.Nterm.
InterPro; IPR003591; LRR.typ.
Pfam; PP00560; LRR; 10.
Pfam; PP01462; LRRCT; 1.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRCT; 1.
SRART; SM00013; LRRCT; 1.
SRART; SM001369; LRRCT; 1.
STGNAL
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STANDARD;
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IPR001611; LRR
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                                                                                                                                                                                                                                                                                                                                                                                                                        215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 YLDRNQLSSYPSAALSKLRVVEELKLSHNPLKSIPDNAFQSFGRYLETLWLDNTNLEKFS 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FACTOR RECEPTOR AND MEDIATES VON WILLEBRAND FACTOR-DEPENDENT PLATELET ADHESION TO BLOOD VESSELS. THE ADHESION OF PLATELETS TO WINURED VASCULAR SURFACES IN THE ARTERIAL CIRCULATION IS A CRITICAL INITIATING ENTER IN HEMOSTASIS (BY SIMILARITY). SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: CONTAINS 14 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                       99 AFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYL 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216 RNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNCDILWLSWWIKDM 275
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                                                                                                              Gaps
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                                                                                                                                                      3 CPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFK-----H 54
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                            34;
                                                                Length 361;
                                                              ; Score 394; DB 1; Length 36; Pred. No. 4.8e-21; 49; Mismatches 139; Indels
  DA79DC98AD3DD1F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Greated)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Platelet glycoprotein V precursor (GPV) (CD42D).
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MEDLINE-97275136; PubMed-9129030;
40884 MW;
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31.9%;
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                                                                                                          Matches 104; Conservative
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  AA;
                                                                                   Best Local Similarity
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361
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008742;
SEQUENCE
                                                                  Query Match
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33 DRIGNESSLTESGNILESEPPALFLHVSSVSRLTLEENPLEEELPDVLFGEMAGLRELWLN 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 RNNLTHLPKGLLGAQVKLEKLLLYSNQLTSVDSGLLSNLGALTELRLERNHLRSVAPGAF 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 NGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLG
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(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 AIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 LERIHLHHNPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDONYFTCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RKNLREVPDGI ---STNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 567;
                                                            14.5%; Score 367; DB 1; Length 567
31.3%; Pred. No. 7e-19;
tive 53; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (PC
N-LINKED (GLCNAC. . .) (PC
N-LINKED (GLCNAC. . .) (PC
C48643AA73967A7D CRC64;
                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GP---EPRASLSFWELLQGDPWCPDPRSL 478
                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED
                                                                                                                                                                                                                      InterPro; IPR000483; LRR_Cterm.
InterPro; IPR00372; LRR_Nterm.
InterPro; IPR003592; LRR_Nterm.
InterPro; IPR003591; LRR_Uty.
Pfam; PF00560; LRR; 13.
Pfam; PF01463; LRR; 11.
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385
567 AA;
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Best Local Similarity
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01-MAR-2002 (Rel. 41, L
Slit protein precursor.
  181
243
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567 AA;
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                                                                                             Query Match
Best Local Simi
Matches 110;
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SLIT_DROME
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                                                                                           Eukaryota, Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                       of functional thrombin cleavage.";

Elood 89:3253-3262(1997).

-I-FUNCTION: THE GPIB-V-IX COMPLEX FUNCTIONS AS THE VON WILLEBRAND FACTOR RECEPTOR AND MEDIATES VON WILLEBRAND FACTOR PECEPTOR AND MEDIATES VON WILLEBRAND FACTOR PLATELET ADHESION TO BLOOD VESSELS. THE ADHESION OF PLATELETS TO INJURED VASCULAR SURFACES IN THE ARTERIAL CIRCULATION IS A CATICAL INTITATING EVENT IN HEMOSTASIS (BY SIMILARITY).

-I-SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                 Ravanat C., Morales M., Azorsa D.O., Moog S., Schuhler S., Grundert P., Low D., van Dorsselaer A., Cazenave J.-P., Lanza F.; Grundert P., I and Mouse platelet glycoprotein V: identification of megakaryocyte specific promoters and demonstration
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SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRNT; 1.
SMART; SM00349; LRR_TPP: 10.
Platelet; Transmembrane; Glycoprotein; Blood coagulation;
Repeat; Leucine rich repeat; Cell adhesion; Signal.
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PLATELET GLYCOPROTEIN V.
EXTRACELLULAR (POTENTIAL).
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                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Platelet glycoprotein V precursor (GPV) (CD42D)
            567 AA.
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                                                                                                                                               STRAIN-WISTAR; TISSUE-Liver;
MEDLINE-97275136; PubMed-9129030;
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            STANDARD;
                                                                                   Rattus norvegicus (Rat).
                                                                                                                                     SEQUENCE FROM N.A.
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CARBOHYD
            GPV_RAT
008770;
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Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda; Insecta:
Pteryota: Neoptera: Endopterygota; Diptera; Brachycera: Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SALPPGMEHGLTELRVLAVHTNALEELPEDALRGLGRURQVSLRHNRLRALPRTLFRNLS 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 PNLTP-----LIKLDELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQ 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLVEINLAHNNLTLLPHDLFTPLHHLERIHLHNPWNCNCDILWLSWWI-----KDM 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PP-----QCNGPESRASLTFWELLQGDQWC--PSSRGLPPDPPTENALKAPDPTQRPN 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 LCLNONQLSFLPANLFSSLGKLKVLDLSRNNLTHLPQGLLGAQIKLEKLLLYSNRLMSLD 210
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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midline
                                                                                                                                                                                                                                                                                                                                                                                                                                                      VCSCSNQFS------KVICV-RKNLREVPDGI---STNTRLLNLHENQIQIIK 48
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-!- FUNCTION: RECESSARY FOR DEVELOPMENT OF MIDLINE GLIA AND COMMISSURAL AND PATHWAYS. SLIT MAY INTERACT WITH EXTRACELULAR MATRIX MOLECULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EXCRETED BY THE MIDLINE GLIA CELLS AND EVENTUALLY DISTRIBUTED ALONG THE AXONS.
SIMILARITY: CONTAINS 7 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 24 LEUCINE-RICH REPEATS (LRR).
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .)
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                                                                                                                                                                                                                                                                                                                                                                                  42;
                                                                                                                                                                                                                                                                                                               Length 567;
                                                                                                                                                                                                                                                                                                                                                                                  163; Indels
                                                                                                                                                                                                           CA10708E0D03707F CRC64;
                                                                                                                                                                                                                                                                                                           14.1%; Score 356; DB 1; 29.9%; Pred. No. 4.3e-18; ive 53; Mismatches 163;
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01-MAR-1992 (Rel. 21, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
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LRR 23.

LRR 24.

EGF-LIKE 1.

EGF-LIKE 2.

EGF-LIKE 3,

EGF-LIKE 4.

EGF-LIKE 5,

EGF-LIKE 6.

EGF-LIKE 6.

EGF-LIKE 6.
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                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
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Matches 109; Conservative
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                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  -1- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK)
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PROSITE; PS01010; ASX_HYDROXYL; 3.

PROSITE; PS01185; CTCK_1, 1.

PROSITE; PS01025; CTCK_2; 1.

PROSITE; PS01025; EGF_1; 7.

PROSITE; PS01186; EGF_2; 5.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS01025; LaM_G_DOMAIN; 1.

Neurogenesis; Glycoprotein; Signal; Alternative splicing; EGF_like domain; Repeat; Leucine-rich repeat.
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laminin_G; 1.
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EGF_CA; 2.
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LRR; 4.
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--- ELDLSGNHLSAIRPGS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning and characterization of the gene encoding the human platelet glycoprotein V. A member of the leucine-rich glycoprotein family cleaved during thrombin-induced platelet activation.";
                           DCTGRRLKEIPRDIPLHTTELLLNDNELGRISSDGLFGRLPHLVKLELKRNQLTGIEPNA 590
                                                                      Lanza F., Morales M., de la Salle C., Cazenave J.-P., Clemetson K.J., Shimomura T., Phillips D.R.;
                                                                                                                 HHNPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVE 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 170:153-161(1990).
-!- FUNCTION: THE GPIB-V-IX COMPLEX FUNCTIONS AS THE VON WILLEBRAND FACTOR RECEPTOR AND MEDIATES VON WILLEBRAND FACTOR-DEPENDENT PLATELET ADHESION TO BLOOD VESSELS. THE ADHESION OF PLATELETS TO INJURED VASCULAR SURFACES IN THE ARTERIAL CIRCULATION IS A
                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE-93391348; PubMed-7690959;
Hickey M.J., Hagen F.S., Yagi M., Roth G.J.;
"Human platelet glycoprotein V: characterization of the polypeptide
and the related Ib-V-IX receptor system of adhesive, leucine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Platelet;
MEDLINE-90321220; PubMed-2372284;
Roth G.J., Church T.A., McMullen B.A., Williams S.A.;
Human platelet glycoprotein V: a surface leucine-rich glycoprotein "elated to adhesion.";
                                                      FQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHL
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-90275263; PubMed-2350580;
Shimomura T., Pujimura K., Maehama S., Takemoto M., Oda K.,
Fujimoto T., Oyama R., Suzuki M., Icihara-Tanaka K., Titani K.,
Kuramoto A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Rapid purification and characterization of human platelet glycoprotein V: the amino acid sequence contains leucine-rich repetitive modules as in glycoprotein Ib."; alood 75:2349-2366(1990).
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                                                                                                                                                                                                                                                              01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Platelet glycoprotein V precursor (GPV) (CD42D).
                                                                                                                                                315 PPADLNVTEGMAAELKCRASTSLTSVSWITPNGTVM 350
                                                                                                                                                                      ----ENSEGCLGDGYCPPSCTCT-----GTVV 726
                                                                                                                                                                                                                              560 AA.
          ---IKLD---
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MEDLINE-94012616; PubMed-8407908;
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01-FEB-1995 (Rel. 31, Last sequal 16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                               STANDARD;
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SWART; SW00309; LRRCT; 1.
SWART; SW00082; LRRCT; 1.
SWART; SW00013; LRRUT; 1.
SWART; SW00089; LRR_TYP; 9.
Platelet; Transmembrane; Glycoprotein; Blood coagulation;
Platelet: Transmembrane; Glycoprotein; Signal.
                                                                              SIMILARITY: CONTAINS 14 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLATELET GLYCOPROTEIN V. EXTRACELULAR (POTENTIAL)
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CRITICAL INITIATING EVENT IN HEMOSTASIS.
SUBCELLULAR LOCATION: TYPE I membrane protein.
TISSUE SPECIFICITY: PLATELETS AND MEGAKARYOCYTES.
PTM: THE N-TERMINUS IS BLOCKED.
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
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                                                                                                                                                                                                                                                                           EMBL; L11238; AAA03069.1; -. EMBL; Z23091; CAA80637.1; -. HSSP; P16473; IXUM.
MIM; 173511; -.
                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00560; LRR; 14.
Pfam; PF01463; LRRCT; 1
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331
331
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109
130
138
209
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Score 329.5; DB 1; Length 560; Pred. No. 3.2e-16;

13.1%;

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                                                                                    LRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNN 114
                                                                                                                     PIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPNLTPL 174
                                                                                                                                                                                                                                                                                                                                                                chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Delhanty P., Baxter R.C.; "The cloning and expression of the baboon acid-labile subunit of the
49; Gaps
                       ----ISTNTRLLN------LHENQIQIIKVNSFKH 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         insulin-like growth factor binding protein complex.";
Biochem. Biophys. Res. Commun. 227:897-902(1996).
-!- FUNCTION: INVOLVED IN PROPEIN PROTEIN INTERACTIONS THAT RESULT IN PROTEIN COMPLEXES, RECRETOR-LIGAND BINDING OR CELL ADHESION.
-!- SUBUNIT: FORMS A TERNARY COMPLEX OF ABOUT 140 TO 150 kDa WITH IGF-I AND IGFEP3 (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: EXCRACellular.
-!- SIMILARITY: CONTAINS 20 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                    175 IKLDELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNN
                                                                                                                                    Papio hamadryas (Hamadryas baboon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NAN-2002 (Rel. 41, Last annotation update)
Insulin-11ke growth factor binding protein complex acid labile precursor (ALS).
Mismatches 104; Indels
                                                                                                                                                                                                                    LTLLPHDLFTPLHHLERIHLHNPWNCNCDILWLSWWIK 273
                                                                                                                                                                                                                                     EMBL; S83462; -; NOT_ANNOTATED_CDS
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43;
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INTERPLO; IPRODO483; LRR_CTERM.
INTERPLO; IPRODO482; LRR_NEFERM.
INTERPLO; IPROD3592; LRR_OUT.
INTERPLO; IPROD3591; LRR_LYP.
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SMART; SM00370; LRR; 2.
Conservative
                                                                                                                                                                                                                                                                                                         STANDARD;
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Pfam; PF01463; LRRCT; 1.
Pfam; PF01462; LRRNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Cercopithecinae; Papio.
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                        NLREVPDG----
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83;
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ID ALS_PAPHA
AC 002833;
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Matches
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                                                                                                                                          BY SIMILARITY.
INSULIN-LIKE GROWTH FACTOR BINDING
PROTEIN COMPLEX ACID LABILE CHAIN.
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SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRNT; 1.
Glycoprotein; Leucine-rich repeat; Repeat; SIGNAL
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01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 41, Last annotation update)
1INSULIN-11N-11Ne growth factor binding protein complex acid labile chain IGFALS OR ALS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 28-35.
MEDLINE-89308584; PubMed-2473065;
Baxter R.C., Martin J.L., Benlac V.A.;
"High molecular weight insulin-like growth factor binding protein '
complex. Purification and properties of the acid-labile subunit from human serum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of
                                                                                                                                                                                                                                                                                                                                                          Homo saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leong S.R., Baxter R.C., Camerato T., Dai J., Wood W.I.; "Structure and functional expression of the acid-labile subunit the insulin-like growth factor-binding protein complex."; Mol. Endocrinol. 6:870-876(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGF-I OR IGF-II AND IGFBP-3.
--- SUBCELLULAR LOCATION: Extracellular.
--- TISSUE SPECIFICITY: PLASMA.
--- SIMILARITY: CONTAINS 20 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                       605 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUE-Liver;
MEDLINE-92357025; Pubmed-1379671;
                                                                                   576 YTYNNITCASPPEVAGLDLRDLGEAHF 602
                                                            286 -----CNTPPNLKGRYIGELDQNYF
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LRR_Nterm.
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InterPro; IPR003591; LRR_typ.
Pfam; PF00560; LRR: 19.
Pfam; PF01463; LRRCT; 1.
Pfam; PF01463; LRRCT; 1.
PRINTS; PR00019; LEURICHRPT.
SWART; SM00370; LRR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL031724; CAC36078.1;
PIR; A41915; A41915.
HSSP; P23945; 1XUN.
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IPR000372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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P35858;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 TIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-501-1994 (Rel. 29, Created)
01-501-1994 (Rel. 29, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 50, Last annotation update)
16-0CT-2001 (Rel. 60, Last annotation update)
16-0CT-2001 (Rel. 70, Last annotation update)
16-0CT-2001 (Rel. 70, Last annotation update)
16-0CT-2001 (Rel. 29, Created)
16-0CT-2001 (Rel. 29, Created)
16-0CT-2001 (Rel. 20, Last annotation update)
16-0CT-2001 (Rel. 20, Last annotation update)
16-0CT-2001 (Rel. 20, Last annotation update)
16-0CT-2001 (Rel. 20, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 NLRYLNLAMCNLREIPN--LTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQI
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..) (POTENTIAL).
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SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_TYP; 11.
Glycoprotein; Leucine_rich repeat; Repeat; Signal.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                           Dai J., Baxter R.C.; Molecular cloning of the acid-labile subunit of the rat insulin-like
                                                                                                                                                                 serum insulin-like growth factor binding protein complex.";
Endocrinology 134:848-852(1994).
-!- FUNCTION: MAY HAVE AN IMPORTANT ROLE IN REGULATING THE ACCESS OF CIRCULATING THE ACCESS OF CIRCULATING THE ACCESS OF CIRCULATING TORMS A TERNARY COMPLEX OF ABOUT 140 TO 150 kDa WITH IGF-I OR IGF-I AND IGFBP-3.
                                                                                                                                                       'Purification and characterization of the acid-labile subunit of rat
                                                                                                                                                                                                                                        TISSUE SPECIFICITY: BRAIN, KIDNEY, LUNG, HEART, SPLEEN, MUSCLE AND LIVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN.
                                                                                                                                                                                                                                                             -!- SIMILARITY: CONTAINS 21 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_TYP; 9.
Glycoprotein; Leucine-rich repeat; Repeat; Signal.
                                                                              growth factor binding protein complex.";
Biochem. Biophys. Res. Commun. 188:304-309(1992)
                                                                                                                                                                                                                              -! - SUBCELLULAR LOCATION: Extracellular.
                                                                                                               SEQUENCE OF 24-44, AND CHARACTERIZATION
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MEDLINE=94130835; PubMed=7507839;
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InterPro; IPR001611; LRR.
InterPro; IPR0001483; LRR_Cterm.
InterPro; IPR001572; LRR_Nterm.
InterPro; IPR001592; LRR_out.
InterPro; IPR001591; LRR_typ.
Pfam; PF00160; LRR; 19.
Pfam; PF001463; LRRCT; 1.
Pfam; PF001463; LRRCT; 1.
Pfam; PF001463; LRRCT; 1.
PR00119; LEURICHPT.
                                         FISSUE=Liver;
MEDLINE=93038676; Pubmed=1384485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; S46785; AAB23770.2; -. PIR; JC1282; JC1282.
HSSP; P23945; 1XUN.
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SMART; SM00082; LRRCT;
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                                                                                                                                              Baxter R.C., Dai J.;
                               SEQUENCE FROM N.A.
         CBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 GLSNLRYLNLAMCNLREI - - PNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKLWMIQ 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         528 ERLWLDANPWDCSCPLKAL ---- RDFALQNPGVVPRFVQTVCEGDDCQPVYTYNNITCAG 583
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NAR-2002 (Rel. 41, Last annotation update)
Insulin-like growth factor binding protein complex acid labile chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 93:10028-10033(1996).
-!- FUNCTION: MAY HAVE AN IMPORTANT ROLE IN REGULATING THE ACCESS CIRCULATING IGFS TO THE TISSUES.
-!- SUBULT: FORMS A TERNARY COMPLEX OF ABOUT 140 TO 150 kDa WITH IGF-I OR IGF-II AND IGFBP-3 (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: CONTAINS 21 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 LLNLH-----ENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDN
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musincel_TaxID=10090;
                                                                                                                   (POTENTIAL).
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LRR 19.

LRR 20.

LRR 21.

N-LINKE 31.

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IGFALS OR ALS OR ALBS.
Mus musculus (Mouse).
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EIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAF---- 219
                                                         HIDLSHNRVAGLLEDTFPGLLGLHVLRLAHNAITSLRPRTFKDLHFLEELQLGHN 324
                                             -----DNLQSLVE-----INLAHNNLTLLPHDLFTPLHHLERIHLHHN 257
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MEDLINE=93162643; PubMed=8432527;
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MEDLINE-93162642; PubMed-8432526;
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MEDLINE-87017013; Pubmed-3484330;
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MEDLINE-87250639; Pubmed-3597437;
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 EMBL outstation
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INSULIN-LIKE GROWTH FACTOR BINDING
PROTEIN COMPLEX ACID LABILE CHAIN.
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and the
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Pred. No. 2.9e-14;
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Swiss Institute of Bioinformatics
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InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR_Cterm.
InterPro; IPR000372; LRR_Nterm.
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LRR_typ.
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Pfam; PF01463; LRRCT; 1.
Pfam; PF01462; LRRNT; 1.
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SMART; SM00013; LRRNT;
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SMART; SM00082; LRRCT;
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TO DECORIN CAN BE EITHER
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J. Biol. Chem. 262:9702-9708 (1987).
-i- FUNCTION: BINDS TO TYPE I AND TYPE II COLLAGEN AND AFFECTS THE RATE OF FIBRILS FORMATION. ALSO BINDS TO FIBROMECTIN AND TGF-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roughley P.J., White R.J.; "Derman articular cartilage. The "Dermatan sulphate proteoglycans of human articular cartilage. The properties of dermatan sulphate proteoglycans I and II."; Blochem. J. 262:823-827(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fisher L.W., Hawkins G.R., Tuross N., Termine J.D.; Purification and partial characterization of small proteoglycans
                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTERNATIVE PRODUCTS: 5 isoforms; A (shown here), B, C, D and are produced by alternative splicing.
                                                                                                                                                                                                                                 Krusius T., Ruoslahti E.;
"Primary Structure of an extracellular matrix proteoglycan core protein deduced from cloned cDNA.";
Proc. Natl. Acad. Sci. U.S.A. 83:7683-7687(1986).
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                                                                                                                                                                                                                                                                                                                                                                                 Vetter U., Vogel W., Just W., Young M.F., Fisher L.W.; "Human decorin gene: intron-exon junctions and chromosomal
P07585; Q9Y5N9; Q9Y5N8; Q9P020; Q9P021;
01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Bone proteoglycan II precursor (PG-S2) (Decorin) (PG40).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS A; B; C; D AND Cs-Szabo G., Glant T.T.; "Alternative splicing of human decorin.";
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Query Match
Best Local Simi
Matches 85;
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N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
MISSING (IN ISOFORM B).
MISSING (IN ISOFORM C).
MISSING (IN ISOFORM C).
LDKV -> CLES (IN ISOFORM E).
MISSING (IN ISOFORM E).
                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Connective tissue; Extracellular matrix; Proteoglycan; Repeat; Leucine-rich repeat; Signal; Alternative splicing;
SIMILARITY: BELONGS TO THE SMALL INTERSTITIAL PROTEOGLYCANS
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/FTId=VAR_011975.
G -> A (IN REF. 6).
D -> P (IN REF. 6).
FF511E871A1A52DD CRC64;
                 SIMILARITY: CONTAINS 10 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                BONE PROTEOGLYCAN II.
                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                              EMBL; M14219; AAB00774.1; ...
EMBL; L01131; AAA52301.1; ALT_SEQ.
EMBL; L01125; AAA52301.1; JOINED.
EMBL; L01126; AAA52301.1; JOINED.
EMBL; L01129; AAA52301.1; JOINED.
EMBL; L01139; AAA52301.1; JOINED.
EMBL; L01130; AAA52301.1; JOINED.
EMBL; M98262; AAB60901.1; ...
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Pfam; PF01462; LRRWT; 1.
SMART; SM00370; LRRR; 3.
SMART; SM0013; LRRRT; 1.
SMART; SM001369; LRR_TYP; 1.
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359 AA;
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*Alternatively spliced version of the porcine decorin gene.";
*Submitted (APR-1999) to the EMBL/Genbank/DDBJ databases.
-- FUNCTION: BINDS TO TYPE I AND TYPE II COLLAGEN AND AFFECTS THE RATE OF FIBRILS FORMATION. ALSO BINDS TO FIBRONECTIN AND TGF-BETA (BY SIMILARITY).
-- PRINT THE GLYCOSAMINOGLYCAN CHAIN ATTACHED TO DECORIN CAN BE EITHER CHONDROTTIN SULFATE OR DEFENDING UPON THE TISSUE OF ORIGIN.
                                                                                                                                                                                                                                                                                                                                                                63 LSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSY 122
                                                                                                                                                                                                            112 LVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPE---KMPKTLQELRAHENEITKVRKV 168
                                                                                                                                                                                                                                                      123 AFNRIPSLRRLDLG--ELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDEL 180
                                                                                                           3 CPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQ 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomí;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE SMALL INTERSTITIAL PROTEOGLYCANS
12.0%; Score 302; DB 1; Length 359; 33.1%; Pred. No. 1.6e-14;
                                         41; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stephenson S., Schnoke M., Vesely I.; "Cloning of the porcine decorin gene."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 10 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9XSD9; Q9XSH4;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CGT-2001 (Rel. 40, Last annotation update)
Bone proteoglycan II precursor (PG-S2) (Decorin);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (SHORT FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (LONG FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR01611; LRR.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003592; LRR_out.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-YORKSHIRE; TISSUE-Aorta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF125537; AAD23578.1; -. EMBL; AF140270; AAD33862.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   287 GL-AEHKYIQVVYLHNN 302
                                                                                                                                                                                                                                                                                                                                                                                                                           241 DLFTPLHHLERIHLHHN 257
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-YORKSHIRE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGS2_PIG
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Eutheria; Perissodactyla; Equidae; Equus.

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NCBI_TaxID=9796;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPFRCQC--HLRVVQCSDLGLDKVPKDLPPDTALLDLQNNKITEIKDGDFKNLKNLHTLI 112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 LINNKISKISPGAFAPLVKLERLYLSKNOLKELPE---KMPKTLOELRVHENEITKVRKA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 DLFTPLHHLERIHLHNPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIG-- 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GL-AEHKYIQVVYLHNN--NISA-----VGSNDFCPPGYNTK---KASYSGVS 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 AFNRIPSLRRIDLG--ELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDEL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 CPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQ
                                                                                                        Extracellular matrix; Proteoglycan;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 40, Last annotation update)
Bone proteoglycan II pescursor (PG-S2) (Decorin) (Dermatan sulfate proteoglycan II) (DS-PGII)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 DLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eŭkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                             . .) (POTENTIAL).
. .) (POTENTIAL).
. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                          LRR 10.
O-LINKED (GLYCOSAMINOGLYCAN) (BY SIMILARITY).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.7%; Score 295; DB 1; Length 360; 30.5%; Pred. No. 5.2e-14; Live 44; Mismatches 139; Indels
                                                                                                                        Signal; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISSING (IN SHORT ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8573DE8DDEBA7509 CRC64;
                                                                                                                                                                       PROTEOGLYCAN II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 AA
                                                                                                                                                       SIMILARITY
                                                                                                                                    POTENTIAL.
BY SIMILAR
BONE PROTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
              Pfam; PF00560; LRR; 9.
Pfam; PF01462; LRRNT; 1.
SWART; SM00130; LRR; 1.
SWART; SM00013; LRRNT; 1.
SWART; SM000189; LRR_TYP; 2.
Glycoprotein; Connective tissue; Ex
Repeat; Leucine-rich repeat; Signal
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LERR
LERR
LERR
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MW.:
InterPro; IPR003591; LRR_typ
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330 LFSNPVQYWEIQPSTFRC 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39899
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Matches 97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             212
263
304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                360 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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31
31
100
1124
1147
1169
2240
2240
287
34
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046542;
                                                                                                                                                                                                                                                                                                                                          REPEAT
CARBOHYD
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SEQUENCE
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REPEAT
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PGS2_HORSE
                                                                                                                                                                       CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                         FUNCTION: BINDS TO TYPE I AND TYPE II COLLAGEN AND AFFECTS THE RATE OF FIBRILS FORMATION. ALSO BINDS TO FIBRONECTIN AND TGF-BETA (BY SIMILARITY).

PTW: THE GLYCOSAMINOGLYCAN CHAIN ATTACHED TO DECORIN CAN BE EITHER CHONDROITIN SULFATE OR DERMATAN SULFATE DEPENDING UPON THE
SEQUENCE FROM N.A.
Richardson D.W., Dodge G.R.;
"Effects of interleukin-1 beta and tumor necrosis factor-alpha on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVNNKISKISPGAFTPLVKLERLYLSKNHLKELPE---KMPKTLQELRVHENEITKVRKA 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Extracellular matrix; Proteoglycan;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . .) (POTENTIAL). . . . (POTENTIAL). . . . (POTENTIAL). . .
                                                                  expression of matrix related genes in cultured equine articular chondrocytes.";
                                                                                                                                                                                                                                                               TISSUE OF ORIGIN (BY SIMILARITY).
SIMILARITY: BELONGS TO THE SMALL INTERSTITIAL PROTEOGLYCANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40;
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O-LINKED (GLYCOSAMINOGLYCAN) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLYCOSAMINOGLYCAN) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.6%; Score 294; DB 1; Length 36(30.4%; Pred. No. 6.1e-14;
tive 44; Mismatches 138; Indels
                                                                                                                     Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: CONTAINS 10 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2DAE97CDE16F7C45 CRC64;
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BONE PROTEOGLYCAN II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal
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LERR 3.
LERR 4.
LERR 5.
LERR 6.
LERR 7.
LERR 8.
LERR 9.
LERR 9.
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ve tissue; F
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InterPro; IPR001611; LRR.
InterPro; IPR00372; LRR_Nterm.
InterPro; IPR003592; LRR_out.
Pfam; PF00560; LRR: 9.
Pfam; PF01462; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
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Repeat; Leucine-rich repeat;
SIGNAL 17
PROPEP 17
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239
263
263
309
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Best Local Similarity
Matches 97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 AA;
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DISULFID
SEQUENCE
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288 GV-ADHKYIQVYLHNN----NISAI-------GSNDFCPPGYNTK---KASYSGVS 329
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01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Bone proteoglycan II precursor (PG-S2) (Decorin).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 LINNKISKISPGAFAPLVKLERLYLSKNQLKELPE---KMPKTLQELRVHENEITKVRKS 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 DLFTPLHHLERIHLHHNPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIG-- 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 CPFRCQC--HLRVVQCSDLGLEKVPKDLPPDTALLDLQNNKITEIKDGDFKNLKNLHTLI 112
              SMART; SM00370; LRR; 2.
SMART; SM0013; LRRUT; 1.
SMART: SM00369; LRR_TYP; 2.
Glycoprotein; Connective tissue; Extracellular matrix; Proteoglycan;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 HLDGNKITKVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHLRELHLNNNKLAKVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 DLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 LSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 AFNRIPSLRRLDLG--ELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDEL
                                                                                                                                                                                                                                                                                                                                                                                                              .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                       (GLYCOSAMINOGLYCAN) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.6%; Score 293; DB 1; Length 36(29.9%; Pred. No. 7.2e-14;
tive 46; Mismatches 139; Indels
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                                                                                                                                                        BONE PROTEOGLYCAN II
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
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BY SIMILAR
BY SIMILAR
                                                                                               Leucine-rich repeat; Signal.
1 16 POTENTIAL.
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LRR 9.
LRR 10.
O-LINKED (
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Best Local Similarity
Matches 95; Conserv
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NCBI_TaxID=9031;
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P28675;
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CARBOHYD
DISULFID
DISULFID
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PGS2_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: THE GLYCOSAMINOGLYCAN CHAIN ATTACHED TO DECORIN CAN BE EITHER CHONDROITIN SULFATE OR DERWATAN SULFATE DEPENDING UPON THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Choi H.U., Johnson T.L., Pal S., Tang L.H., Rosenberg L., Neame P.J.; "Characterization of the dermatan sulfate proteoglycans, DS-PGI and DS-PGII, from bovine articular cartilage and skin isolated by octyl-
                                                                                                                                                                                               287 GGL-ADHKYIQVVYLHNN--NISA------VGSNDFCPPGYNTK---KASYSGV 328
                                                                                                                                                                      240 HDLFTPLHHLERIHLHHNPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIG- 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sepharose chromatography.";
J. Biol. Chem. 264:2876-288(1989).
-!- FUNCTION: BINDS TO TYPE I AND TYPE II COLLAGEN AND AFFECTS THE RATE OF FIBRILS FORMATION. ALSO BINDS TO FIBRONECTIN AND TGF-
                                    AFNRIPSLRRLDLG--ELKRLSYISEGAFEGLSNLRYLNLAMCNLREI-PNLTPLIKLDE
                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                           LDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE SMALL INTERSTITIAL PROTEOGLYCANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
MEDLINE-88133946; PubMed-3435485;
Day A.A., McQuillan C.I., Termine J.D., Young M.R.;
"Molecular cloning and sequence analysis of the cDNA for small proteoglycan II of boxine bone.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: CONTAINS 10 LEUCINE-RICH REPEATS (LRR)
                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
16-C7T-2001 (Rel. 40, Last annotation update)
Bone proteoglycan II precursor (PG-S2) (Decorin).
                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. J. 248:801-805(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Y00712; CAA68702.1; -.
                                                                                                                                                                                                                                                   ------ELDQNYFTC 307
                                                                                                                                                                                                                                                                                        329 SLFSNPVQYWEIQPSTFRC 347
                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00560; LRR; 9.
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B31430; B31430.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            taurus (Bovine).
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SEQUENCE OF 31-54.
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10;

Gaps

180

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                          -i- PTM: THE GLYCOSAMINOGLYCAN CHAIN ATTACHED TO DECORIN CAN BE EITHER CHOONDOITH SULFATE OR DERMATAN SULFATE DEDENDING UPON THE TISSUE OF ORIGIN (BY SIMILARITY)
-i- SIMILARITY: BELONGS TO THE SMALL INTERSTITIAL PROTEOGLYCANS
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InterPro; IPR001611; LRR.
InterPro; IPR000312; LRR_Uterm.
InterPro; IPR003592; LRR_Out.
InterPro; IPR003592; LRR_Lyp.
Pfam; PF00460; LRR; 10.
SMART; SM00170; LRR; 1.
SMART; SM001013; LRRWT; 1.
SMART; SM0018; LRRWT; 1.
SMART; SM0018; LRRWT; 1.
SMART; SM0018; LRRWT; 1.
SMART; SM0018; LRRWT; 1.
SMART; SM00189; LRR_TYP; 2.
SMART; SM00169; LRRWT; 1.
SMART; SM00169; LRRWT; 1.
SMART; SM00169; LRRWT; 1.
SMART; SM00169; LRRWT; 1.
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                            LI W., Vergnes J.P., Cornuet P.K., Hassel J.R.;
"cDNA clone to chick corneal chondroitin/dermatan sulfate
proteoglycan reveals identity to decorin.";
Arch. Blochem. Blophys. 296:190-197(1992).
-1- FUNCTION: BINDS TO TYPE I AND TYPE II COLLAGEN AND AFFECTS THE
RATE OF FIBRILS FORMATION. ALSO BINDS TO FIBRONECTIN AND TGF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LER 10.
O-LINKED (GLYCOSAMINOGLYCAN) (BY SIMILARITY)
N-LINKED (GLCNAC. ...) (POTENTIAT)
N-LINKED (GLCNAC. ...) (POTENTIAT)
BY SIMILARITY.
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STRAIN-WHITE LEGHORN; TISSUE-Cornea;
MEDLINE-92296755; PubMed-1605630;
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Best Local Similarity
Matches 85; Conserv
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RESULT
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O9hcj2 homo sapien
O96a85 homo sapien
O9nt99 homo sapien
O9bc20 homo.sapien
O96fe5 homo.sapien
O9fe5 homo sapien
O9fe6 homo sapien
O96ni6 homo sapien
O9430 drosophila
O43377 homo sapien
O9h38 homo sapien
O9bja homo sapien
O9bja homo sapien
O9bja homo sapien
                                                                                        August 26, 2002, 15:46:18; Search time 31.39 Seconds (without alignments) 2634.329 Million cell updates/sec
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1 QTCPSVCSCSNQFSKVICVR......KTFTIPVTDINSGIPGIDEV 478
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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sp_invertebrate:*
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Maximum DB seq length: 200000000
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sp_rodent:*
sp_virus:*
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Match Length DB
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P97860 Q9BE71 Q9ULH4 Q9CYK3 P70193 Q96RJ5	Q61809 073675 015335 09ESY6 09WVB5 Q9DE37	0981189 055226 095710 095710 094813 09WUG5 092626	0/0210 09BTN0 09WVC1 09V738 075093 094898
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707 789 832 788 1091 359 492	716 718 359 707 1531 1515	1521 358 358 1521 1521 1529 1525 1496	358 628 796 1173 1534 1065 660
16.2 16.2 16.1 15.0 15.9 15.9	15.8 15.8 15.7 15.7 15.6		112.0 112.0 124.0 144.0 14.0 14.0
410 408 406 406 402.5 401.5	398.5 398.3 397.5 393.5 389.5	388333 38833 3883 3873 3873 3873 3873 3	382.5 380 377.5 377 377 376
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ALIGNMENTS

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471 GI-PGIDEV 478
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Wang J., Bin L., Jiang N., Li G.;
"Homo sapiens brain-specific gene (BAG), downregulated in brain tumor,
mRNA.";
                                                                                                                                     240
                                                                                                                                                                                                                                                                      LOLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIP 120
                                                                                                                                                                        SYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDEL 180
                                                                                                                                                                                                                                              DQNYFTCYAPVIVEPPADLNVTEGMAAELKCRASTSLTSVSWITPNGTVMTHGAYKVRIA 360
                                                                                                                                                                                                                                                                                                                    361 VLSDGTLNFTNVTVQDTGMYTCMVSNSVGNTTASATLNVTAATTTPFSYFSTVTVETMEP 420
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                 421 SQDEARTTDNNVGPTPVVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEV 478
                                                                                                                                                                                                                                                                                                                                                                                           DLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPH
                                                                                                                           QTCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Usukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OCBI_TaxID=9606;
                                                                                                         ö
                                                                                         640;
                                                                                        Length
                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases EMBL, AF196976; AAG28019.2; -. HSSP; P23945; 1XUN.
                                                             6058974872636838 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
U-CCT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BRAIN TUMOR ASSOCIATED PROTEIN NAG14.
                                                                                       Score 2524; DB 4;
Pred. No. 1.8e-181;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               653 AA
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                                                             640 AA; 71949 MW;
                                                                                      100.0%;
ilarity 100.0%;
Conservative 0
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Interpro; IPR003598; Ig.c2.
Interpro; IPR003600; Ig_L1ke.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR001611; IRC.
SM00410; IG_11ke; 1.
       SMART; SM00370; LRR; 6.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_TYP; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                            Immunoglobulin domain.
                                                                                       Query Match
Best Local Similarity
Matches 478; Conserv
                                                    NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLSDGTLNFTNVTVQDTGMYTCMVSNSVGNTTASATLNVTAA--TTTPFSYFSTVTVETM 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QTCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEI
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                         38159C81F6850E37 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 72.3 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 62.7%; Score 1581.5; DB 4; Local Similarity 60.9%; Pred. No. 1.3e-110; nes 298; Conservative 77; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR00352; LRR_Out.
InterPro; IPR003591; LRR_LYP.
Ffam; PF00047; 19; 1.
Ffam; PF001463; LRRCT; 1.
Ffam; PF01462; LRRCT; 1.
Ffam; PF01462; LRRCT; 1.
SWART; SW00409; IG, 1.
SWART; SW00409; IG, 1.
SWART; SW00082; LRRCT; 1.
SWART; SW00082; LRRCT; 1.
SWART; SW00082; LRRCT; 1.
SWART; SW00082; LRRCT; 1.
SWART; SW00081; LRRCT; 1.
SWART; SW00082; LRRCT; 1.
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InterPro; IPR000483;
InterPro; IPR003592;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DONYFICYAPVIVEPPADLNVTEGMAAELKCRASTSLTSVSWITPNGTVMTHGAYKVRIA 360
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                                                                                                                                                                                                                                                                                                                                                          LQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIP 120
                                                                                                                                                                                                                                     25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ol-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 15, Last sequence update)
HYPOTHETICAL 45.1 KDA PROTEIN (FRAGMENT).
DKFZP76AA179.
HOMO sapiens (Human).
EUKALYOCA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                           1 QTCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blum H., Bauersachs S., Mewes H.W., Gassenhuber J., Wiemann S.; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL137451; CAB70743.1; -.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MKC.
InterPro; IPR0011611; LRR.
                                   Wang J.;
Thesis 2000), Zhongshan Medical University, Guangzhou, China.
EMBL: 3A299858; CAC82651.1; -.
Signal; Hypothetical protein.
The potential protein.
                                                                                                                                                                                           61.7%; Score 1556.5; DB 4; Length 60.5%; Pred. No. 9.4e-109;
                                                                                                                                                                                                                                     Indels
                                                                                                                POTENTIAL.
9C11C5ABC7E536CF CRC64;
                                                                                                                                                                                                                                       93;
                                                                                                                                                                                                                                   75; Mismatches
                                                                                                                                 72313 MW;
                                                                                                                                                                                                                                       Conservative
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                                                                                                                                 SEQUENCE 649 AA;
                                                                                                                                                                                                                  Similarity
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TISSUE-AMYGDALA;
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                SEQUENCE FROM N.A.
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Best Local Simi
Matches 296;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 MCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDN 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCARCNTPPNLKGRY IGELDQNYFTCYAPVIVEPPADLNVTEGMAAELKCRASTSLTSVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51; Indels
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"Brain tumor-associated mRNA.";
"Brain tumor-associated mRNA.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF290542; AAG60620.1;
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR0031611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45110 MW; 164C6AF1A4BC440C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 45.6%; Score 1151.5; DB 4
Best Local Similarity 59.8%; Pred. No. 1.5e-78;
Matches 213; Conservative 53; Mismatches 51;
InterPro; IPR000483; LRR_Cterm.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_tout.
InterPro; IPR000317; Tubulin.
Pfam; PF00047; ig; 1.
Pfam; PF00463; LRR; 3.
Pfam; PF00463; LRR; 3.
Pfam; PF00469; LRR; 1.
SMART; SM00089; LRRCT; 1.
SMART; SM00082; LRRCT; 1.
SMART; M00082; LRRCT; 1.
SMART; SM00369; LRRCT; 1.
SMART; SM00370; LRR; 1.
SMART; SM00000; LRR; 1.
SMART; SM00000; LRR; 1.
SMART; SM000000; LRR; 1.
SMART; SM000000; LRR; 1.
SMART; SM0000000; LRR; 1.
SMART; LRR; 1.
SMART
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRR_Cterm.
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Immunoglobulin domain.
SEQUENCE 606 AA; 68
                                                                                                                                                                                                                                                                   SMART;
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Q96FE5
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Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
Hotutanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
                                                                                                                                                                                                                                                                            170 NLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEIN 229
                                                                                                                                                                                                                                                                                                                                                                          MTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGNTTASATLNVTAA--TTTPF 407
                                                                                                                                                                                                                                                                                                                                                                                                                         SYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQSTRSTEKTFTIPVTD 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
8438B23.1 (NEGRONAL LEGIOINE-RICH REPEAT PROTEIN) (CDNA FLJ31810 FIS, CLONE NT2R12009289, WEAKLY SIMILAR TO CARBOXYPEPTIDASE N 83 KDA
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                            PNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAELKCRASTSLTSVSWITPNGTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                34.6%; Score 872.5; DB 11; Length 441; 52.2%; Pred. No. 1.4e-57; Live 57; Mismatches 87; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Babbage A.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                             441 AA; 48844 MW; E2D17AB4607AC475 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        606 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
           Pfam; PF00047; ig; i. Pfam; PF00560; LRR; 2. Pfam; PF0463; LRRCT; 1. SMART; SM00409; IG; 1. SMART; SM00410; IG_Like; 1. SMART; SM00370; LRR; 2. SMART; SM00082; LRRCT; 1. InterPro; IPR003591; LRR_typ
                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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TTDKMQTSLDEV 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      468 INSGI-PGIDEV 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                             Best Local Sim
Matches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BA438B23.1.
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SEQUENCE
                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             381 -MCAGPDTIRERSFKDFHSTALSFYFTCKKPKIREKKLQHLLVDEGQTVQLECSADGDPQ 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              440 PVISWVTPRRRFITTKSNG----RATVLGDGTLEIRFAQDQDSGMYVCIASNAAGNDTFT 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 CPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQ 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSDNIIANVEPGAFNNLFNLRSLRLKGNRLKLVPLGVFTGLSNLTKLDISENKIVILLDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 HLKHLNINNMPVYAFKRLFHLKHLEIDYWPLLDMMPANSLYGLNLTSLSVTNTNLSTVPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----LIKLDELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         284 ARCNTPPNLKGRYIGELDQN----YFTCYAPVIVEPPAD-LNVTEGMAAELKCRASTSLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                339 SV-SWITPNG---TVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGNTTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLAHNNLTLLPHDLFTPLHHLERIHLHNPWNCNCDILWL----SWWIKDMAPSNTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  395 ATLNVTAATTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSL 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 AFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAMCNLREIP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----NLTP----
human cDNA sequencing project.";
:ted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CB608E281B066B9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.4%; Score 565.5; DB 4;
29.3%; Pred. No. 2.6e-34;
ive 79; Mismatches 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ¥.
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01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                                                                                   InterPro; IPR001611, LRR.
InterPro; IPR001611, LRR.
InterPro; IPR000483; LRR. Cterm.
InterPro; IPR000372; LRR.Nterm.
InterPro; IPR003591, LRR.Ltyp.
Pfam; PF00047; ig; 1.
Pfam; PF001660; LRR; 11.
Pfam; PF01463; LRRY; 1.
Pfam; PF01463; LRRY; 1.
PRNUNS; PR00019; LEURICHRPT.
SMART; SM00408; IGc2; 1.
SMART; SM00408; IGc2; 1.
SMART; SM00018; LRRY; 1.
                  Submitted (OCT-2001) to the EMI
EMBL; AL353746; CAC22713.1; -.
EMBL; AK056372; BAB71167.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68065 MW;
                                                                                              InterPro; IPR003599; Ig.
InterPro; IPR003598; Ig.c2.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SM00369; LRR_TYP; 10.
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Best Local Similarity 29.3%
Matches 157; Conservative
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63 LSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao Suzuki Y., Sugano S., Hashimoto K.;
**Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 CPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215 RLRHLNINAIRDYSFKRLYRLKVLEISHWPYLDTMTPNCLYGLNLTSLSITHCNLTAVPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----LIKLDELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNCDILWL---SWWIKDMAPSNTACCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286 CNTPPNLKGRYIGE----LDQNYFTCYAPVIVEPPA-DLNVTEGMAAELKCRA-STSLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 450 ILWLSPRKHLVS-AKSNGRLTVFPDGTLEVRYAQVQDNGTYLCIAANAGGNDSMPAHLHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LNENIVSAVEPGAFNNLFNLRTLGLRSNRLKLIPLGVFTGLSNLTKLDISENKIVILLDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 AFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAMCNLREIP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      335 NVSGNQLTTLEESVFHSVGNLETLILDSNPLACDCRLLWVFRRRWRLNFNRQQPT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    340 VSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGNTTASATLNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 400 TA-ATTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSL 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 22.2%; Score 560.5; DB 6; Length Best Local Similarity 30.3%; Pred. No. 6.3e-34; Matches 161; Conservative 74; Mismatches 203; Indels
                                                                                                   to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin domain.
187 MW; BA6C8BC7C993BE9A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ä.
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                                                                                                                                                                      Interpro; IPR003598; Ig_c2.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR001611; ILRR.
Interpro; IPR000483; ILR_Cterm.
Interpro; IPR000372; ILR_NETER.
Interpro; IPR003592; ILR_Out.
Interpro; IPR003591; ILR_Ltyp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69187 MW;
                                                                             libraries.";
Submitted (JUL-2000) to the
EMBL; AB046639; BAB03557.1;
HSSP; P23945; 1XUN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SM00369; LRR_TYP; 1.
                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 1.
Pfam; PF00560; LRR; 9.
Pfam; PF01463; LRRCT; 1.
Pfam; PF01462; LRRUT; 1.
SMART; SW00408; IGC2; 1.
SMART; SM00370; LRR; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00082; LRRCT; 1.
SM00013; LRRNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein;
SEQUENCE 614 AA; 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART;
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Q9D1T0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 LSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.3
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQ 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286 CNTPPNLKGRYIGE----LDQNYFTCYAPVIVEPPA-DLNVTEGMAAELKCRA-STSLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | || ::|: | || |||| | : | || || || CATPEFVQGKEFKDFPDVLPNYFTCRRARIRDRKAQQVFVDEGHTVQFVCRADGDPPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215 RLRHLNINAIRDYSFKRLYRLKVLEISHWPYLDTMTPNCLYGLNLTSLSITHCNLTAVPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----LIKLDELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NLAHNNLTLLPHDLFTPLHHLERIHLHNPWNCNCDILWL---SWWIKDMAPSNTACCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340 VSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGNTTASATLNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE-BRAIN, AND ANAPLASTIC OLIGODENDROGLIOMA WITH 1P/190 LOSS;
                                                                                                                                                                                                                                                                                                                                                                                                                                       93;
                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           400 TA-ATTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSL 449
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                                                                                                                                                                                                                                     Strausberg R.;
Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011057; AAH11057.1; -.
SEQUENCE 614 AA; 69145 MW; EFD967E3B716698D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 69.2 KDA PROTEIN.
(TrEMBLrel. 19, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                       74; Mismatches 202;
                                                                                                                                                                                                                                                                                                                                                                                   22.4%; Score 565.5; DB 4
Llarity 30.5%; Pred. No. 2.7e-34;
Conservative 74; Mismatches 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
    01-DEC-2001 (TrEMBLrel. 19, Last
01-DEC-2001 (TrEMBLrel. 19, Last
UNKNOWN (PROTEIN FOR MGC:17422).
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TISSUE=CEREBELLUM CORTEX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cercopithecinae; Macaca
                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 162; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-9541;
                                                                                                                                                NCBI_TaxID=9606;
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| | || ::|: : | ||||| | : | : | || || : || 390 CATPEFVQGKEFKDFPDVLLPNYFTCRRAHIRDRKAQQVFVDEGHTVQFVCRADGDPPPA 449
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                            215 RLRHLNINAIRDYSFKRLYRLKVLEISHWPYLDTMTPNCLYGLNLTSLSITHCNLTAVPY 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 VDLTLSRNTISFITPHAFADLRNLRALHLNSNRLTKITNDMFSGLSNLHHLILNNNQLTL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokol T., Kodaira H., Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamanoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Marsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai T.; Isogai T.;
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                                                                                                ILWLSPRKHLVS-AKSNGRLTVFPDGTLEVRYAQVQDNGTYLCIAANAGGNDSMPAHLHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 QICPKRCVCQILSPNLATLCAKKGLLFVPPNIDRRTVELRLADNFVTNIKRKDFANMTSL
                                                                                                                                                                 NLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNCDILWL---SWWIKDMAPSNTACCAR
                                                                                                                                                                                           286 CNTPPNLKGRYIGE----LDQNYFTCYAPVIVEPPA-DLNVTEGMAAELKCRA-STSLTS
                                                                                                                                                                                                                                                                                                                                                     340 VSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGNTTASATLNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 IPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLL
                                                                          ----LIKLDELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ30803 FIS, CLONE FEBRA2001245, WEAKLY SIMILAR TO NAG14.
                                                                                                                                                                                                                                                                                                                                                                                                                                           400 TA-ATTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSL 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 17.9%; Score 453; DB 4; Length 719; Best Local Similarity 27.7%; Pred. No. 9.4e-26; Matches 137; Conservative 61; Mismatches 210; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "NEDO human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AK055365; BAB70910.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               719 AA; 79472 MW; CE301F219705FF4B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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Substant Carractor No. 1

Substant Carractor No. 1

Rawal J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawal J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Antawa T., Hara A., Eukunishi Y., Konno H., Adachi J., Fukuda S., Antawa T., Hara A., Ishik K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R., Ashburner M., Batalov S., Casyant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casyant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casyant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casyant T., Radota K., Matsudi F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Ashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodríguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whynshaw-Bonis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Narandi V., Narandi H., Rohtsuki S., Narandia V., Kawaji H., Rohtsuki S., Narandia V., Rawaji W., Rawaji W., Rawadia V., Rawaji W., Rawaji W., Rawaji W., Rawaji W., Rawaji W., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 CPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQ 62
                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNENIVSAVEPGAFNNLFNLRTLGLRSNRLKLIPLGVFTGLSNLTKLDISENKIVILLDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11; Length 614;
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ADDLT ALE TESTIS CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLONE: 4930471R13, FULL INSERT SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA; 69100 MW; 41CFF40C21335681 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.2%; Score 559.5; DB 1.
llarity 30.3%; Pred. No. 7.5e-34;
Conservative 73; Mismatches 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRR_Cterm.
LRR_Nterm.
LRR_typ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR003599; Ig.
IPR003598; Ig.c2.
IPR003600; Ig.like.
IPR003006; Ig.MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409:685-690(2001).
EMBL; AK027262; BAB32403.1; -.
HSSP; P23945; 1XUN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; SM00409; IG; 1.
; SM00408; IGC2; 1.
; SM00410; IG_like; 1.
; SM00082; IRRCT; 1.
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Pfam; PF00560; LRR; 9.
Pfam; PF01463; LRRCT; 1.
Pfam; PF01462; LRRNT; 1.
                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000372;
InterPro; IPR003591;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047;
Pfam; PF00560; 1
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Best Local Simi
Matches 161;
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RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
Raderige R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Tandell M.D., Zhang Q., Chen L.X.,
Raticon G.G., Wortman J.R., Palazej R.G., Champe M., Pfelifer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.,
RA Adril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Adril J.F., Doyle C., Baxradale J., Bayraktaroglu L., Beasley E.M.,
RA Adril J.F., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.C.,
RA Butis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley D.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Godson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
Adodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.L.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
A Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
A Mantel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J.J., Ma. M.-H., Ibegwam C.,
A Mattel B.C., Mattel B., McIntosh T.C., McLeod M.P., Mcoherson D.L.
RA Mantel B.C., Mattel B., McIntosh T.C., McLeod M.P., Mcoherson D.L.
RA Merkulov G., Milshian N.V., Mobarry C., McLeod M.P., Moshrefi A.,
Rainer B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Standers R., Venter E., Wang A.,
Wang Z.-Y., Wassarman D.A., Weilsecher E., Spradling A.C., Standers E., Wang A.,
Walliams S.M., Woodage T., Worley C., Wu D., Yang S., Yao Q., Zhen G.,
Williams S.M., Woolage T., Worley C., Wang S., Yao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEEKS OR BG:DS04862.1 OR CG4192.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                        | | | : : | | | : : | | : : | 376 KLPHLLNSTNHIHEPDPGSSDISTSTSTRSGSNT----SSSNGDTKLSQDKIVVAEATSST 430
                                                                 RCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAELKCRA-STSLTSVSWI 343
                                                                                    TPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGNTTASATLNVTAAT 403
                                                                                                                                                                                                     TTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQSTRSTEKTFTI 463
 --HLHHNPWNCNCDILWLSWWIKDMAPSNTACCA 284
                                 PPD----PLFQRAQVLATSGIISPSTFALSFGGNPLHCNCELLWL-----RRLSREDDLE
                                                                                                                                                                   SPEGKLISNA - - TRSLVYDNGTLDILITTVKDTGAFTCIASNPAGEATQIVDLHI - - - I
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1021 AA.
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431 ALLKFNFORNIPGI 444
PHDLFTPLHHLERI --
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Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O., Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; science 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 IPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHDLFTPLHHLERIHLHHNPWNCNCDILWL-SWWIKDMAPSNTACCARCNTPPNLKGRYI 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G., Butenhoff C., Champe M., Chavez C., Chew M., Clesiolka L., Doyle C.M. Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A., Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Nebresi M.A., Mazda P., Moshrefi A.R., Moshrefi M., Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A., Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 CPSVCSCSNQFSK--VICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSF--KHLRHL 58
                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=Y, AND CN BW SP;
MEDLINE=99403001; PubMed=10471707;
MEDLINE=99403001; PubMed=10471707;
MSSTRAIN=Y, Mistra S., Roote J., Lewis S.E., Blazej R., Davis T.,
Boyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
Palazzaolo M., Rese M.G., Spradling A., Tsang G., Wan K., Whitelaw F.
An exploration of the sequence of a 2.9-Mb region of the genome of
Drosophila melanogaster: the Adh region.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1021;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AE003648; AAF53467.1; -.
EMBL; AE003413; AAF4948.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.6%; Score 443.5; DB 5
30.0%; Pred. No. 7.8e-25;
iive 54; Mismatches 144
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InterPro; IPR003508; Ig_C2.
InterPro; IPR0031006; Ig_MHC.
InterPro; IPR00111; LRR.
InterPro; IPR001683; LRR_Cterm.
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InterPro; IPR000483; LRR_Cter
InterPro; IPR003592; LRR_Nter!
InterPro; IPR003592; LRR_Lout.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01463; LRRCT; 1.
SMART; SM00408; IGC2; 1.
SMART; SM00370; LRR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=Y, AND CN BW SP;
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Pfam; PF00560; LRR; 6.
Pfam; PF01463; LRRCT; 1
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Best Local Similarity
Matches 127; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00013;
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217 NAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNCDILWLSW---WIK 273
                                                                                                                                                                              274 DMAPSNTACCARCNTPPNLKGRYIGELD-QNYFTCYAPVIVEP--PADLNVTEGMAAELK 330
                                                                                                                                                                                                                                               331 CRASTS-LTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVG 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN-3).
DKF2P761K2424 OR NLRR-3.
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                               SGNHLSAIRPGSFQGLMHLQKLWM------IQS------QIQVIER
                                                                                                                                             325 NAFFRLPKLESLMLNSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMKTNIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-WAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 79.4 KDA PROTEIN (NEURONAL LEUCINE-RICH REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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Hypothetical protein; Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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LRR_out.
LRR_typ.
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InterPro; IPR003598; 19_c2.
InterPro; IPR003006; 19_MHC.
InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PR00019; LEURICHRPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00041; fn3; 1... Pfam; PF00047; 1g; 1... Pfam; PF00560; LRR; 9... Pfam; PF01463; LRRCT; 1... Pfam; PF01462; LRRNT; 1...
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SMART; SM00409; IG; 1.
SMART; SM00408; IGC2; 1.
SMART; SM00370; LRR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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InterPro; IPR003591;
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InterPro; IPR000483;
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                                                                                                                                                                                                                                                                                                              390 NTTASATLNV 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Q9H3W5
Q9H3W5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART;
SMART;
                                                                                                                                                                                                              385
                 205
                                               183
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                                     86 DFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLEENKLTELPEKCLSELSNLQELYIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 DNRLTTIPNGAFVYLSKLKELMLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 FEGLSNLRYLNLAMCNLREIPN-----------LTPLIKLDELDL 182
                                                                                ----YKVRIAVLSDG-----TLNFTNVTV----QDTGMYTCMVSNSVGNTTASAT 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 CPSVCSCS------NQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIK--- 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 CPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQTNNIAKIEYST 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---SFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELF 88
                 GELDQNYFICYAPVIVEPPADLNVTEGMAAELKCRA-STSLTSVSWITPNGTVMTHGA--
                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98;
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P SEQUENCE FROM N.A.

C TISSUE-FIBROBLAST:

A MURRAY J., Langston Y., Clarke C.;

RL Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.

BR InterPro; IPR003961; FN_III.

DR InterPro; IPR003968; Ig_C2.

DR InterPro; IPR0031698; Ig_C2.

DR InterPro; IPR001611; LRR.

InterPro; IPR001611; LRR.

InterPro; IPR0004037; LRR_Cterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.7%; Score 421; DB 4; Length 705; 27.1%; Pred. No. 2.3e-23; tive 74; Mismatches 185; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA; 79049 MW; 9B46066693F4BC1A CRC64;
                                                                                                                                                                                                                                                                                                          01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROBABLE LEUCINE-RICH REPEAT PROTEIN.
                                                                                                                                                                                                                                                                705 AA
                                                                                                                                                                                                                                                                                                Created)
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Pfam; PF00560; LRR; 9.
Pfam; PF01463; LRRCT; 1.
Pfam; PF01462; LRRWT; 1.
PRINTS; PR00019; LEURICHRPT.
                                                                                                                                                                                                                                                                                             01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00408; IGC2; 1.
SMART; SM00370; LRR; 4.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRWT; 1.
SMART; SM00369; LRR_TYP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin domain.
SEQUENCE 705 AA; 79
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                 397 LNVT 400
                                                                                                                                                                              LAVS 429
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Matches 133;
                                                                                                                                                                                                                                                                                                                                                               RG118D07.1
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---YAFNRIPSLRRLDLGELKRL-- 141
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                                                                                                                                                                                                                                                                                                 PRT;
 NGAFVYLSKLKELWLRNNPIESIPS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00369; LRR_TYP; 14.
Immunoglobulin domain.
SEQUENCE 1094 AA; 119165 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000483; LRR_Cterm.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003592; LRR_out.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR003591; LRR_typ. 10047; ig; 3. 10560; LRR; 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01463; LRRCT; 1.
Pfam; PF01462; LRRNT; 1.
PRINTS; PR00019; LEURICHRPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SM00410; IG_like; 1.
SM00370; LRR; 5.
SM00082; LRRCT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM00013; LRRNT; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGc2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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SMART;
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                                                                                                                                                                                                                                                                                                                  NAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNCDILWLSW---WIK 273
                                                                                                                                                                                                                                                                                                                                                                  274 DMAPSNTACCARCNTPPNLKGRYIGELD-QNYFTCYAPVIVEP--PADLNVTEGMAAELK 330
                                                                                                                                                                                                                                                                                                                                                                                 .----- LTPLIKLDELDL 182
                                                                                                                                                                                                                                      331 CRASTS-LTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVG 389
                                                                                                                                                                                                                                                                                                                                                                                                                              89 DNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGA 148
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIEP, 96
                                                                                                        88
                                                                                3 CPSVCSCS-----NQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIK--- 48
                                                                                                     29 CPRICTCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQTNNIAKIEYST
                                                                                                                               49 ---VN-------SFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                          98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.4%; Score 413.5; DB 4; Length 1093; 28.3%; Pred. No. 1.5e-22; tive 78; Mismatches 170; Indels 73;
                                  Length 708;
                               Query Match
16.7%; Score 421; DB 4; Length 70
Best Local Similarity 27.1%; Pred. No. 2.3e-23;
Matches 133; Conservative 74; Mismatches 185; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8488FA41BB10F353 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nilsson J., Vallbo C., Henriksson R., Hedman H.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF381545; AAK62357.1;
SEQUENCE 1093 Aa; 119052 MW; 8488FA41BB10F353 CRC64;
24710478D6B124D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MEMBRANE GLYCOPROTEIN LIG-1.
                                                                                                                                                                                                                          FEGLSNLRYLNLAMCNLREIPN---------
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79424 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             390 NTTASATLNV 399
 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    504 ADLKSVMIKV 513
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Best Local Similarity
Matches 127; Conserv
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708
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 SEQUENCE
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364
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                                                                                                                                                                                                                                                                                                               254 LHHNPWNCNCDILWLSWWI--KDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTC---Y 308
                                                                                                                                                                                          194 SFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIH
                                                                                              309 APVIVEPPADLNVTEGMAAELKCRASTSLTS---VSWITPNGTVMTHGAYKVRIAV-LSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G-----TLNFTNVTVQDTGMYTCMVSNSVGNT---TASATLNVTAA-TTTPFSYFSTV
276 SGSLYGLTALHQLHLSNNSIARIHRKGWSFCQKLHELVLSFNNLTRLDEESLAELSSLSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      494 KPQIITQPETTMAMVGKDIRFTCSAASSSSSPMTFAWKKDN-EVLTNADMENFVHVHAQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suzuki Y.;
"human membrane glycoprotein LIG-1.";
Submitted (CCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB050468; BAB40659.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MEMBRANE GLYCOPROTEIN LIG-1.
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15;
                                                                                                                                                                                                                            97 NGAFVYLSKLKELWLRNNPIESIPS------YAFNRIPSLRRLDLGELKRL-- 141
                                                                                                                                                                                                                                                                                                                                                                                                                  | | |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----SYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDELDLSGNHLSAIRPG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 SFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIH 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 LHHNPWNCNCDILWLSWWI--KDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTC---Y 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 APVIVEPPADLNVTEGMAAELKCRASTSLTS---VSWITPNGTVMTHGAYKVRIAV-LSD 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G-----TLNFTNVTVQDTGMYTCMVSNSVGNT---TASATLNVTAA-TTTPFSYFSTV 413
                                                                                           Gaps
                                                                                                                                                                            37 LNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIP 96
                                                                                               73;
    Length 1094;
                                                                                           Indels
Query Match 16.4%; Score 413.5; DB 4; Best Local Similarity 28.3%; Pred. No. 1.5e-22; Matches 127; Conservative 78; Mismatches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TVETMEPSQDEARTTDNNVGPTPVVDWE 441
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Search completed: August 26, 2002, 15:50:24 Job time: 246 sec

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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/FOMB.pep:*
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          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-103-950-2
US-09-191-647-7
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US-09-540-153-7
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Sequence 2, P
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APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: EXTRACELLULAR ADHESIVE PROTEINS
FILE REFERENCE: PF-0576 US
CURRENT APPLICATION NUMBER: US/09/131,648
CURRENT FILING DATE: 1998-08-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PERL Program
SEQ ID NO 2
LENGTH: 708
US-08-442-063A-48
US-08-441-063A-27
US-08-619-916-2
US-08-619-916-2
US-08-30-238-4
US-08-30-238-4
US-08-4186-834-4
5340934-4
5340934-4
5340934-4
US-08-916-918-7
US-08-9119-268-6
US-08-119-268-6
US-08-119-268-6
US-08-119-268-6
US-08-113-929A-11
US-08-214-265A-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09131648; Patent No. 6168920; GENERAL INFORMATION: APPLICANT: Hillman, Jennifer L.
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US-09-131-648-2
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Sequence Sequence Sequence

US-08-190-802A-50 US-08-477-346-50 US-08-473-089-50 US-08-986-485-6 US-08-442-063A-45

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  278 SGSLYGLTALHQLHLSNNSISRIQRDGWSFCQKLHELILSFNNLTRLDEESLAELSSLSI 337
                                                                                                                        194 SFQCLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIH
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                                                                                                                                                                                                       254 LHHNPWNCNCDILWLSWWI--KDMAPSNTACCARCNTPPNLKGRYI-GELDQNY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: WU, SHUJIAN
APPLICANT: SWEET, RAYMOND
APPLICANT: TRUNEH, ALEMSEGED
TITLE OF INVENTION: A HUMAN LIG-1 HOMOLOG (HLIG-1)
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAINER & PRESTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70264
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JMBER: US/08/986,485
08-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,448
FILING DATE: 22-SEP-1997
ATTORNEY/AGENT INFORMATION:
                                                                  Sequence 2, Application US/08986485
Patent No. 6046030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    435 TPVVDWETTNVTTSLT 450
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723 TPRITWLKGGRPLSLT 738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   610-407-0701
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VALLEY FORGE
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COMPUTER READABLE FORM:
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APPLICANT: WU, SH
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                                                                                                                                  CRASTS-LISVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVG 389
DMAPSNTACCARCNTPPNLKGRYIGELD-QNYFTCYAPVIVEP--PADLNVTEGMAAELK 330
                                                                                                                                                                         NGAFVYLSKLKELWLRNNPIESIPS-----141
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                                                                                   388 FMEPDSLFCV----DPPEFGGQNVRQVHFRDMMEICLPLIAPESFPSNLNVEAGSYVSFH
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Patent No. 6046030
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: WWW, SHUJIAN
APPLICANT: TRUNEH, ALEMSEGED
TITLE OF INVENTION: A HUMAN LIG-1 HOMOLOG (HLIG-1)
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77; Mismatches 168;
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SOFTWARE: FastERO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,485
FILING DATE: 08-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,448
FILING DATE: 22-SEP-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-7-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0701
TELEFAX: 610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
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INFORMATION FOR SEQ ID NO: 5:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-986-485-5
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STRANDEDNESS: si
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Best Local Similarity
Matches 134; Conserv
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DG-----TLNFTNVTVQDTGMYTCMVSNSVGNT---TASATLNVTAA-TTTPFSYFST 412
                                                                                                                                                                                                                                                                                                                                                                                               142 -----SYISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDELDLSGNHLSAIRPG 193
                                                                                                                                                                                                                                                                                                                                                                                                                       SFQGL-MHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERI 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HLHHNPWNCNCDILWLSWWI--*KDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTC--- 307
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                                                                                                                                                                                                             Gaps
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APPLICANT GOODING.
APPLICANT GOODING.
APPLICANT ENOSE, KALJA
APPLICANT TESSIET-LAVIGNE, MATC
TITLE OF INVENTION: MODULATING RODO: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/191,647
CURRENT PILING DATE: 1996-11-13
EARLIER PLING DATE: 1997-11-14
EARLIER PILING DATE: 1997-11-14
EARLIER PLING DATE: 1998-04-07
EARLIER FILING DATE: 1998-04-07
SOFTWARE: PATENTING DAYE: 1998-04-07
                                                                                                                                                                                                           Indels
                                                                                                                                                                    Ouery Match 15.6%; Score 393; DB 3; I
Best Local Similarity 27.8%; Pred. No. 3.2e-24;
Matches 125; Conservative 79; Mismatches 171;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-191-647-2; Sequence 2, Application US/09191647; Patent No. 6046015
                   1101 amino acids
SEQUENCE CHARACTERISTICS
                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
NOLECULE TYPE: protein
US-08-986-485-2
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US-09-191-647-2
                   LENGTH:
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                                                                                                                                                                              84 LQLMENKISTIERGAFQDLKELERLRLNRNHLQLFPELLFLGTAKLYRLDLSENQIQAIP 143
                  Gaps
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                                                        QTCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEI 60
                                                                                                26 QACPAQCSCSG--STVDCHGLALRSVPRNIPRNTERLDLNGNNITRITKTDFAGLRHLRV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 TFRLHSNNLYCDCHLAWLSDWLRKRPRVGLYTQCMGPSHLRGHNVAEVQKREFVCSDEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 MIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNCDI
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Best Local Similarity 25.0%; Pred. No. 2e-23;
Matches 124; Conservative 48; Mismatches 164; Indels 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Goodman, Corey
APPLICANT: Goodman, Corey
APPLICANT: Brose, Katja
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REPRENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,245A
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/065,544
PRIOR FILING DATE: 1997-11-14
PRIOR FILING DATE: 1997-11-14
PRIOR FILING DATE: 1997-04-07
                                                                                                                                                                                                                      SYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNL------
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Best Local Similarity
Matches 124; Conserva
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US-09-540-245A-2
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LENGTH: 1525
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	Qy 161 160	Db 203 TFRLHSNNLYCDCHLAWLSDWLRKRPRVGLYTQCMGPSHLRGHNVAEVQKREFVCSDEEE 262	Qy 161AMC	Db 263 GHQSFMAPSCSVLHCPAACTCSNNIVDCRGKGLTEIPTNLPETITEIRLEQNTIKVIPPG 322	QY 171 -LTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKLW 205	Db 323 AFSPYKKLRRIDLSNNQISELAPDAFQGLRSLNSLVLYGNKITELPKSLFEGLFSLQLLL 382	Qy 206 MIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNCDI 265	Db 383 LNANKINCLRVDAFQDLHNLNLLSLYDNKLQTIAKGTFSPLRAIQTMHLAQNPFICDCHL 442	Qy 266 LWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGM 325	Db. 443 KWLADYL-HINPIETS-GARCTSPRRLANKRIGQIKSKKFRCSGTEDYRSKLSGDCFADL 500	Qy 326 AAELKCRASTSLTSVS 341	Db 501 ACPEKCRCEGTTVDCS 516	RESULT: 7	08-09-182-024A-2	sequence 2, Application 05/031820248 : Patent No. 6342370	: GENERAL INFORMATION: : APPLICANT: Connolly, Timothy	: APPLICANT: Rajput, Bhanu ; TITLE OF INVENTION: Human Slit Polypeptide and Polynucleotides Encoding		CURRENT APPLICATION NUMBER: US/09/182,024A	PRIOR APPLICATION NUMBER: 60/063,946	PRIOR APPLICATION NUMBER: 60/096,420	: PRIOR FILING DATE: 1998-08-13 : NUMBER OF SEO ID NOS: 5	SOFTWARE: PatentIn Ver. 2.1	SEQ 10 NO 2 LENGTH: 1523	TYPE: PRT ORGANISM: Homo sapiens	US-U9-182-024A-Z	14.7%; Scc 24.6%; Pre	132; Conservative 56; Mismat	QY 3 CPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQ 62	DD 34 CPTKCTCSAASVDCHGLGLRAVPRGIPRNAERLDLDRNNITRITKMDFAGLKNLRVLH 91	63 LSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELMLRNNPIESIPSY	DD 92 LEDNYVSVIERGARQULKQLEKLKKUNNNKLQVLPELLFQSIPKLIKKULSENQIQGIPKK 151 OV 103 ABNUTDGI DBIDIGEIKDI GVIGEGARFGI GNI BVINI	152 AFRICTION/MICHIEL III 1 1 1 1 1 1 1 1 1	161	Db 211 RLHSNHLYCDCHLAWLSDWLRQRRTVGQFTLCMAPVHLRGFNVADVQKKEYVCPAPHSEP 270	
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QY 61 LQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTIPNGAFVYLSKLKELMLRNNPIESIP 120	DD 84 LQLMENKISTIERGAFQDLKELERLKINRNHLQLFPELLFLGTAKLYRLDLSENQIQAIP 143	SEGAFEGLS	Db 144 RKAFRGAVDIKNLQL-DYNQISCIEDGAFRALRDLEVLTLNNNNITRLSVASFNHMPKLR 202	Фу 161 160	Db 203 TFRLHSNNLYCDCHLAWLSDWLRKRPRVGLYTQCMGPSHLRGHNVAEVQKREFVCSDEEE 262	Qy 161	Db 263 GHQSFWAPSCSVLHCPAACTCSNNIVDCRGKGLTEIPTNLPETITEIRLEQNTIKVIPPG 322	SNHLSAIRPG	DD 323 AFSPYKKLRRIDLSNNQISELAPDAFQCLRSLNSLVLYGNKITELPKSLFEGLFSLQLLL 382	QY 206 MIQSQIQVIERNAFDNLOSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHPWNCNCDI 265	DEHNINILSLYDNKLQTIAKGTFSPLRAIQTMHLAQNPFI	266 LWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGM	Db 443 KWLADYL-HTNPIETS-GARCTSPRRLANKRIGQIKSKKFRCSGTEDYRSKLSGDCFADL 500	Qy 326 AAELKCRASTSLTSVS 341	Db 501 ACPEKCRCEGTTVDCS 516		RESULT 6 US-09-540-153-2	Sequence 2, Application US/09540153 Patent No. 6270995	GENERAL INFORMATION: APPLICANT: Goodman, Corey	Kid, Thor	APPLICANT: Tessier-Lavigne, Marc	TITLE OF INVENTION: MODULATING KODO: LIGAND INTERACTIONS FILE REFERENCE: B98-031-3	= 2	PRIOR APPLICATION NUMBER: 09/191, 647		FRIOK FILING DATE: 1998-04-0/ NUMBER OF SEQ ID NOS: 14 SOFTWARE: PATENTIN VET. 2.0	2 1525	TYPE: P	US-09-540-153-2		Query Match 15.3%; Score 386; DB 4; Length 1525; Action of the sest Local Similarity 25.0%; Pred. No. 2e-23; Adatches 124; Conservative 48; Mismatches 164; Indels 160; Gaps	QY 1 QTCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEI 60	CSCSGSTVDCHGLALRSVPRNIPRNTER	OY 61 LQLSRNHIRTIEIGAENGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIP 120	121	

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                                FTPLHHLERIHLHHNPWNCNCDI 265
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FSPLRAIQTMHLAQNPFICDCHL 442
                                                                                  NYFTCYAPVIVEPPADLNVTEGM 325
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9e-22;
173; Indels 176; Gaps
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KKFRCSGTEDYRSKLSGDCFADL 500
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                                                                                                                                                                                                                                                                                                           APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
FILE OF INVENTION: THEREFOR
FILE REPERENCE: MEI-019
CURRENT APPLICATION NUMBER: US/09/063,950C
CURRENT FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
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                                                          IQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHNPWNCNCDILWLSW 270
                                                                                                         WIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAELK 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHNPWNCNCDILWLSWWIKD-- 274
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 ----TPL 174
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                                                                                                                                                                                       64;
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                                              175 IKLDELDLSGNHLSAIRPGSFQ------
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-09-063-950-2
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Matches 115;
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161 AMCN-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----RHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLT--TIP 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.0%; Score 354; DB 4; Length 649; 24.6%; Pred. No. 2.7e-21; ive 88; Mismatches 202; Indels 126;
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                                                                                                                                                                                                                                    APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 305
                     ; Sequence 305, Application US/09188930A
; Patent No. 6150502
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                                                                                                               APPLICANT: Watson, James D. APPLICANT: Strachan, Lorna APPLICANT: Sleeman, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 24.6
Matches 136; Conservative
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                                                                                         GENERAL INFORMATION:
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; ORGANISM: Mouse
US-09-188-930-305
US-09-188-930-305
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US-09-191-647-7
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60/065,544

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TYPE: PRT
ORGANISM: Drosophila melanogaster
PRIOR APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     471 PIETSGARCESPKRMHRRRIESLREEKFKCSWGELRMKLSGECRMDSDCPAMCHCEGTTV 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 -----EIPNLTPL-----IKLD------ELDLSGNHLSAIRPGS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHL 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294 SCPHPCRCADGI - - VDCREKSLISVPVILPDDITDVRLEQNFITELPPKSFSSFRRLRRI 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 QLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPS 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 13.9%; Score 350; DB 3; Length 1480; Best Local Similarity 23.9%; Pred. No. 1.9e-20; Matches 109; Conservative 65; Mismatches 152; Indels 130;
                                                                    APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robe: Ligand Interactions
TITLE OF INVENTION: Modulating Robe: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/191,647
CURRENT FILING DATE: 1998-11-13
EARLIER FILING DATE: 1997-11-14
EARLIER FILING DATE: 1997-11-14
EARLIER FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 7
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kid, Thomas Japplicant: Kid, Thomas Japplicant: Brose, Katja APPLICANT: Brose, Katja APPLICANT: Tessier-Lavigne, Marc TITLE OF INVENTION: Modulating Robo: Ligand Interactions FILE REPERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,245A
CURRENT FILING DATE: 2000-03-31
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                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Drosophila melanogaster US-09-191-647-7
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                GENERAL INFORMATION:
APPLICANT: Goodman, Corey
APPLICANT: Kid, Thomas
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APPLICANT: GOODMAN,
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US-09-540-245A-7
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62 QLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPS 121
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GENERAL INC. 82.70937

APPLICANT: Goodman, Corey

APPLICANT: Kid, Thomas

APPLICANT: Brose, Katja

APPLICANT: Tessier-Lavigne, Marc

TITLE OF INVENTION: Modulating Robo: Ligand Interactions

FILE REFERENCE: B98-031-3

CURRENT APPLICATION NUMBER: US/09/540,153

CURRENT FILING DATE: 2000-03-31

PRIOR FILING DATE: 1998-11-13

PRIOR FILING DATE: 1998-11-13

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.0
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PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION UNMBER: 60/081,057
PRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1480
                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-540-245A-7
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GENERAL INFORMATION:
APPLICANT: Rothberg, Jonathan Marc and Artavanis-Tsakonas, Spyridon
TITLE OF INVENTION: Purified SLIT protein and Sequence Elements Thereof
                                                                                                                                                                                                                                                                                          471 PIETSGARCESPKRMHRRRIESLREEKFKCSWGELRMKLSGECRMDSDCPAMCHCEGTTV 530
                                                                                                                                                                                                                                                                                                                                                                                                                                      651 ASNPFNCNCHLAWFAECVRKKSLNGGA--ARCGAPSKVRDVQIKDLPHSEFKCSS---- 703
                                                                                                                                                                                                                   ------EIPNLTPL------IKLD------ELDLSGNHLSAIRPGS 194
                                                                                                                                                          294 SCPHPCRCADGI--VDCREKSLTSVPVTLPDDTTDVRLEQNFITELPPKSFSSFRRLRRI 351
                                                                                                                                                                                              62 QLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPS 121
                                                                                                                        2 TCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEIL 61
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                                                                                      Indels 130;
                                                                                                                                                                                                                                                                    122 YAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAM------CNLR-----
                                                      Length 1480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     800 Kb storage
                                                                                      65; Mismatches 152;
                                                    Score 350; DB 4;
Pred. No. 1.9e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Barth, Richard J.
REGISTRATION NUMBER: 28,180
REFERENCE/DOCKET NUMBER: 900964/RSB
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/07/624,135
FILING DATE: 7-DEC-1990
ATTORNEY/AGENT INFORMATION:
                                                  13.9%;
23.9%;
                                                                                      Conservative
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                                                  Query Match
Best Local Similarity
Matches 109; Conserv
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US-09-540-153-7
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471 PIETSGARCESPKRMHRRRIESLREEKFKCSWGELRMKLSGECRMDSDCPAMCHCEGTTV 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DD: similarity to epidermal growth Involvement in receptor-ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Tandem EGF-like repeats
LOCATION: 911 to 1150
COTENTION: 911 to 1150
OTHER INFORMATION: protein protein interactions
NAME/KEY: 7th EGF-like repeat
LOCATION: 1353 to 1393
DEBRITFICATION METHOD: similarity to epidermal growth
                                                                                                                                                                                                                                                                                                 similarity to other signal
                                                                                                                                                                                                                                                                                                                                                                                            DD: Array of Flank-LRR-Flank
mediates adhesive events
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.9%; Score 350; DB 5; L 23.9%; Pred. No. 1.9e-20; Live 65; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: developmentally regulated NAME/KEY: COOH-terminal region LOCATION: 1405 to 1480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Alternative splice segment LOCATION: 1394 to 1404 IDENTIFICATION METHOD: experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   experimental
                                                                                                                                                                                                                                                                                                                                                          North ...
LOCATION: 37 to ...
LOCATION: 37 to ...
OTHER INFORMATION: mediates adhesi
...vr/KEY: Tandem EGF-like repeats
                                                                                                                                                                                                                                           NAME/KEY: signal sequence LOCATION: 1 to 36
                                                                                                                         1480 amino acids
TELEPHONE: (212) 972-14C
TELEFAX: (212) 370-1622
TELEX: 236268
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                               IDENTIFICATION METHOD:
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                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
                                                                                                                                                AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 109; Conserva
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Townsend and Townsend Khourie and Crew
                379 Lytton Avenue
      STREET: 3/2 CITY: Palo Alto
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                                                                                        APPLICANT: Connolly, Timothy
APPLICANT: Rajput, Bhanu
TITLE OF INVENTION: Human Slit Polypeptide and Polynucleotides Encoding
TITLE OF INVENTION: Same
FILE REFERENCE: 640100-271
CURRENT APPLICATION NUMBER: US/09/182,024A
CURRENT APPLICATION NUMBER: 60/063,946
PRIOR PILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/063,946
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-13
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APPLICANT: Lanza, Francois
APPLICANT: Cazenave, Jean-Pierre
APPLICANT: Cazenave, Jean-Pierre
APPLICANT: Platelet Glycoprotein V Gene and Uses
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       315 PPADLNVTEGMAAELKCRASTSLTSVSWITPNGTVM 350
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                                 Sequence 5, Application US/09182024A Patent No. 6342370
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08592500; Patent No. 6005089; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              Patentin Ver. 2.1
                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1480
                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-182-024A-5
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                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
SEQ ID NO 5
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55 LRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNN 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 LPNLSSLTLSRNHLAFLPSALFLHSHNLTLLTLFENPLAELPGVLFGEMGGLQELWLNRT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 PIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYLNLAMCNLREIPNLTPL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 IKLDELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNN 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 NLREVPDG ------LISTNTRLLN------LHENOIQIIKVNSFKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 560;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.1%; Score 329.5; DB 3; 29.7%; Pred. No. 2.4e-19; ive 43; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 LTLLPHDLFTPLHHLERIHLHHNPWNCNCDILWLSWWIK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       399 LETLPGDVFGALPRLTEVLLGHNSWRCDCGLGPFLGWLR 437
                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,455
FILING DATE: 09-UUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTATION NUMBER: 29,684
REGISTATION NUMBER: 29,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: August 26, 2002, 15:46:38 Job time: 170 sec
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 12
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEO ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 29.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   560 amino acids
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